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(54) **Title:** MOLECULES FOR DISEASE DETECTION AND TREATMENT

(57) **Abstract:** The present invention provides purified disease detection and treatment molecule polynucleotides (mddt). Also encompassed are the polypeptides (MDDT) encoded by mddt. The invention also provides for the use of mddt, or complements, oligonucleotides, or fragments thereof in diagnostic assays. The invention further provides for vectors and host cells containing mddt for the expression of MDDT. The invention additionally provides for the use of isolated and purified MDDT to induce antibodies and to screen libraries of compounds and the use of anti-MDDT antibodies in diagnostic assays. Also provided are microarrays containing mddt and methods of use.

MOLECULES FOR DISEASE DETECTION AND TREATMENT

TECHNICAL FIELD

The present invention relates to molecules for disease detection and treatment and to the use of these sequences in the diagnosis, study, prevention, and treatment of diseases associated with, as well as effects of exogenous compounds on, the expression of molecules for disease detection and treatment.

BACKGROUND OF THE INVENTION

The human genome is comprised of thousands of genes, many encoding gene products that function in the maintenance and growth of the various cells and tissues in the body. Aberrant expression or mutations in these genes and their products is the cause of, or is associated with, a variety of human diseases such as cancer and other cell proliferative disorders. The identification of these genes and their products is the basis of an ever-expanding effort to find markers for early detection of diseases, and targets for their prevention and treatment.

For example, cancer represents a type of cell proliferative disorder that affects nearly every tissue in the body. A wide variety of molecules, either aberrantly expressed or mutated, can be the cause of, or involved with, various cancers because tissue growth involves complex and ordered patterns of cell proliferation, cell differentiation, and apoptosis. Cell proliferation must be regulated to maintain both the number of cells and their spatial organization. This regulation depends upon the appropriate expression of proteins which control cell cycle progression in response to extracellular signals such as growth factors and other mitogens, and intracellular cues such as DNA damage or nutrient starvation. Molecules which directly or indirectly modulate cell cycle progression fall into several categories, including growth factors and their receptors, second messenger and signal transduction proteins, oncogene products, tumor-suppressor proteins, and mitosis-promoting factors. Aberrant expression or mutations in any of these gene products can result in cell proliferative disorders such as cancer. Oncogenes are genes generally derived from normal genes that, through abnormal expression or mutation, can effect the transformation of a normal cell to a malignant one (oncogenesis). Oncoproteins, encoded by oncogenes, can affect cell proliferation in a variety of ways and include growth factors, growth factor receptors, intracellular signal transducers, nuclear transcription factors, and cell-cycle control proteins. In contrast, tumor-suppressor genes are involved in inhibiting cell proliferation. Mutations which cause reduced or loss of function in tumor-suppressor genes result in aberrant cell proliferation and cancer. Thus a wide variety of genes and their products have been found that are associated with cell proliferative disorders such as cancer, but many more may exist that are yet to be discovered.

DNA-based arrays can provide a simple way to explore the expression of a single polymorphic gene or a large number of genes. When the expression of a single gene is explored, DNA-based arrays are employed to detect the expression of specific gene variants. For example, a p53 tumor suppressor gene array is used to determine whether individuals are carrying mutations that predispose them to cancer. A cytochrome p450 gene array is useful to determine whether individuals have one of a number of specific mutations that could result in increased drug metabolism, drug resistance or drug toxicity.

DNA-based array technology is especially relevant for the rapid screening of expression of a large number of genes. There is a growing awareness that gene expression is affected in a global fashion. A genetic predisposition, disease or therapeutic treatment may affect, directly or indirectly, the expression of a large number of genes. In some cases the interactions may be expected, such as when the genes are part of the same signaling pathway. In other cases, such as when the genes participate in separate signaling pathways, the interactions may be totally unexpected. Therefore, DNA-based arrays can be used to investigate how genetic predisposition, disease, or therapeutic treatment affects the expression of a large number of genes.

The discovery of new molecules for disease detection and treatment satisfies a need in the art by providing new compositions which are useful in the diagnosis, study, prevention, and treatment of diseases associated with, as well as effects of exogenous compounds on, the expression of molecules for disease detection and treatment.

SUMMARY OF THE INVENTION

The present invention relates to human disease detection and treatment molecule polynucleotides (mddt) as presented in the Sequence Listing. The mddt uniquely identify genes encoding structural, functional, and regulatory disease detection and treatment molecules.

The invention provides an isolated polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). In one alternative, the polynucleotide comprises a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104. In another alternative, the polynucleotide comprises at least 30 contiguous nucleotides of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; b) a polynucleotide comprising a naturally occurring polynucleotide comprising a polynucleotide

sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). In another alternative, the polynucleotide comprises at least 60 contiguous nucleotides of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; b) a polynucleotide comprising a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). The invention further provides a composition for the detection of expression of disease detection and treatment molecule polynucleotides comprising at least one isolated polynucleotide comprising a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d); and a detectable label.

The invention also provides a method for detecting a target polynucleotide in a sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence of a polynucleotide selected from the group consisting of SEQ ID NO:1-104; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). The method comprises a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

The invention also provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). The method comprises a)

hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide, and b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof. In one alternative, the invention provides a composition comprising a target polynucleotide of the method, wherein said probe comprises at least 30 contiguous nucleotides. In one alternative, the invention provides a composition comprising a target polynucleotide of the method, wherein said probe comprises at least 60 contiguous nucleotides.

The invention further provides a recombinant polynucleotide comprising a promoter sequence operably linked to an isolated polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). In one alternative, the invention provides a cell transformed with the recombinant polynucleotide. In another alternative, the invention provides a transgenic organism comprising the recombinant polynucleotide.

The invention also provides a method for producing a disease detection and treatment molecule polypeptide, the method comprising a) culturing a cell under conditions suitable for expression of the disease detection and treatment molecule polypeptide, wherein said cell is transformed with a recombinant polynucleotide, said recombinant polynucleotide comprising an isolated polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; iii) a polynucleotide complementary to the polynucleotide of i); iv) a polynucleotide complementary to the polynucleotide of ii); and v) an RNA equivalent of i) through iv), and b) recovering the disease detection and treatment molecule polypeptide so expressed. The invention additionally provides a method wherein the polypeptide has an amino acid sequence selected from the group consisting of SEQ ID NO:105-208.

The invention also provides an isolated disease detection and treatment molecule polypeptide (MDDT) encoded by at least one polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104. The invention further provides a method of screening for a test compound that specifically binds to the polypeptide having an amino acid sequence selected

from the group consisting of SEQ ID NO:105-208. The method comprises a) combining the polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208 with at least one test compound under suitable conditions, and b) detecting binding of the polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208 to the test compound, thereby identifying a compound that specifically binds to the polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208.

The invention further provides a microarray wherein at least one element of the microarray is an isolated polynucleotide comprising at least 30 contiguous nucleotides of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). The invention also provides a method for generating a transcript image of a sample which contains polynucleotides. The method comprises a) labeling the polynucleotides of the sample, b) contacting the elements of the microarray with the labeled polynucleotides of the sample under conditions suitable for the formation of a hybridization complex, and c) quantifying the expression of the polynucleotides in the sample.

Additionally, the invention provides a method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). The method comprises a) exposing a sample comprising the target polynucleotide to a compound, b) detecting altered expression of the target polynucleotide, and c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

The invention further provides a method for assessing toxicity of a test compound, said method comprising a) treating a biological sample containing nucleic acids with the test compound; b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a

polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; iii) a polynucleotide complementary to the polynucleotide of i); iv) a polynucleotide complementary to the polynucleotide of ii); and v) an RNA equivalent of i) through iv). Hybridization occurs under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104; iii) a polynucleotide complementary to the polynucleotide of i); iv) a polynucleotide complementary to the polynucleotide of ii); and v) an RNA equivalent of i) through iv), and alternatively, the target polynucleotide comprises a polynucleotide sequence of a fragment of a polynucleotide selected from the group consisting of i-v above; c) quantifying the amount of hybridization complex; and d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

The invention further provides an isolated polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208. In one alternative, the invention provides an isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:105-208.

The invention further provides an isolated polynucleotide encoding a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208. In one alternative, the polynucleotide encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:105-208. In another alternative, the polynucleotide comprises a polynucleotide sequence selected from the group consisting of SEQ ID

NO:1-104.

Additionally, the invention provides an isolated antibody which specifically binds to a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208.

The invention further provides a composition comprising a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, and a pharmaceutically acceptable excipient. In one embodiment, the composition comprises a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208. The invention additionally provides a method of treating a disease or condition associated with decreased expression of functional MDDT, comprising administering to a patient in need of such treatment the composition.

The invention also provides a method for screening a compound for effectiveness as an agonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting agonist activity in the sample. In one alternative, the invention provides a composition comprising an agonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with decreased expression of functional MDDT, comprising administering to a patient in need of such treatment the composition.

Additionally, the invention provides a method for screening a compound for effectiveness as

an antagonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting antagonist activity in the sample. In one alternative, the invention provides a composition comprising an antagonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with overexpression of functional MDDT, comprising administering to a patient in need of such treatment the composition.

The invention further provides a method of screening for a compound that modulates the activity of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:105-208. The method comprises a) combining the polypeptide with at least one test compound under conditions permissive for the activity of the polypeptide, b) assessing the activity of the polypeptide in the presence of the test compound, and c) comparing the activity of the polypeptide in the presence of the test compound with the activity of the polypeptide in the absence of the test compound, wherein a change in the activity of the polypeptide in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide.

DESCRIPTION OF THE TABLES

Table 1 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with the sequence identification numbers (SEQ ID NO:s) and open reading frame identification numbers (ORF IDs) corresponding to polypeptides encoded by the template ID.

Table 2 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with their GenBank hits (GI Numbers), probability scores, and functional annotations

corresponding to the GenBank hits.

Table 3 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with polynucleotide segments of each template sequence as defined by the indicated "start" and "stop" nucleotide positions. The reading frames of the polynucleotide segments and the Pfam hits, Pfam descriptions, and E-values corresponding to the polypeptide domains encoded by the polynucleotide segments are indicated.

Table 4 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with polynucleotide segments of each template sequence as defined by the indicated "start" and "stop" nucleotide positions. The reading frames of the polynucleotide segments are shown, and the polypeptides encoded by the polynucleotide segments constitute either signal peptide (SP) or transmembrane (TM) domains, as indicated. For TM domains, the membrane topology of the encoded polypeptide sequence is indicated as being transmembrane or on the cytosolic or non-cytosolic side of the cell membrane or organelle.

Table 5 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with the component sequence identification spans (component spans) corresponding to each template. The component sequences, which were used to assemble the template sequences, are defined by the spans indicating the nucleotide positions along each template.

Table 6 shows the tissue distribution profiles for the templates of the invention.

Table 7 shows the sequence identification numbers (SEQ ID NO:s) corresponding to the polypeptides of the present invention, along with the reading frames used to obtain the polypeptide segments, the lengths of the polypeptide segments, the "start" and "stop" nucleotide positions of the polynucleotide sequences used to define the encoded polypeptide segments, the GenBank hits (GI Numbers), probability scores, and functional annotations corresponding to the GenBank hits.

Table 8 summarizes the bioinformatics tools which are useful for analysis of the polynucleotides of the present invention. The first column of Table 8 lists analytical tools, programs, and algorithms, the second column provides brief descriptions thereof, the third column presents appropriate references, all of which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score, the greater the homology between two sequences).

DETAILED DESCRIPTION OF THE INVENTION

Before the nucleic acid sequences and methods are presented, it is to be understood that this invention is not limited to the particular machines, methods, and materials described. Although particular embodiments are described, machines, methods, and materials similar or equivalent to these embodiments may be used to practice the invention. The preferred machines, methods, and materials set forth are not intended to limit the scope of the invention which is limited only by the appended claims.

The singular forms "a", "an", and "the" include plural reference unless the context clearly dictates otherwise. All technical and scientific terms have the meanings commonly understood by one of ordinary skill in the art. All publications are incorporated by reference for the purpose of describing and disclosing the cell lines, vectors, and methodologies which are presented and which might be used in connection with the invention. Nothing in the specification is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

Definitions

As used herein, the lower case "mddt" refers to a nucleic acid sequence, while the upper case "MDDT" refers to an amino acid sequence encoded by mddt. A "full-length" mddt refers to a nucleic acid sequence containing the entire coding region of a gene endogenously expressed in human tissue.

"Adjuvants" are materials such as Freund's adjuvant, mineral gels (aluminum hydroxide), and surface active substances (lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, and dinitrophenol) which may be administered to increase a host's immunological response.

"Allele" refers to an alternative form of a nucleic acid sequence. Alleles result from a "mutation," a change or an alternative reading of the genetic code. Any given gene may have none, one, or many allelic forms. Mutations which give rise to alleles include deletions, additions, or substitutions of nucleotides. Each of these changes may occur alone, or in combination with the others, one or more times in a given nucleic acid sequence. The present invention encompasses allelic mddt.

An "allelic variant" is an alternative form of the gene encoding MDDT. Allelic variants may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. A gene may have none, one, or many allelic variants of its naturally occurring form. Common mutational changes which give rise to allelic variants are generally ascribed to natural deletions, additions, or substitutions of

nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

"Altered" nucleic acid sequences encoding MDDT include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polypeptide the same as MDDT or a polypeptide with at least one functional characteristic of MDDT. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding MDDT, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding MDDT. The encoded protein may also be "altered," and may contain deletions, insertions, or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent MDDT. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of MDDT is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, and positively charged amino acids may include lysine and arginine. Amino acids with uncharged polar side chains having similar hydrophilicity values may include: asparagine and glutamine; and serine and threonine. Amino acids with uncharged side chains having similar hydrophilicity values may include: leucine, isoleucine, and valine; glycine and alanine; and phenylalanine and tyrosine.

"Amino acid sequence" refers to a peptide, a polypeptide, or a protein of either natural or synthetic origin. The amino acid sequence is not limited to the complete, endogenous amino acid sequence and may be a fragment, epitope, variant, or derivative of a protein expressed by a nucleic acid sequence.

"Amplification" refers to the production of additional copies of a sequence and is carried out using polymerase chain reaction (PCR) technologies well known in the art.

"Antibody" refers to intact molecules as well as to fragments thereof, such as Fab, $F(ab')_2$, and Fv fragments, which are capable of binding the epitopic determinant. Antibodies that bind MDDT polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or peptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

The term "aptamer" refers to a nucleic acid or oligonucleotide molecule that binds to a specific molecular target. Aptamers are derived from an <u>in vitro</u> evolutionary process (e.g., SELEX (Systematic Evolution of Ligands by EXponential Enrichment), described in U.S. Patent No.

5,270,163), which selects for target-specific aptamer sequences from large combinatorial libraries. Aptamer compositions may be double-stranded or single-stranded, and may include deoxyribonucleotides, ribonucleotides, nucleotide derivatives, or other nucleotide-like molecules. The nucleotide components of an aptamer may have modified sugar groups (e.g., the 2'-OH group of a ribonucleotide may be replaced by 2'-F or 2'-NH_2), which may improve a desired property, e.g., resistance to nucleases or longer lifetime in blood. Aptamers may be conjugated to other molecules, e.g., a high molecular weight carrier to slow clearance of the aptamer from the circulatory system. Aptamers may be specifically cross-linked to their cognate ligands, e.g., by photo-activation of a cross-linker. (See, e.g., Brody, E.N. and L. Gold (2000) J. Biotechnol. 74:5-13.)

The term "intramer" refers to an aptamer which is expressed in vivo. For example, a vaccinia virus-based RNA expression system has been used to express specific RNA aptamers at high levels in the cytoplasm of leukocytes (Blind, M. et al. (1999) Proc. Natl Acad. Sci. USA 96:3606-3610).

The term "spiegelmer" refers to an aptamer which includes L-DNA, L-RNA, or other left-handed nucleotide derivatives or nucleotide-like molecules. Aptamers containing left-handed nucleotides are resistant to degradation by naturally occurring enzymes, which normally act on substrates containing right-handed nucleotides.

"Antisense sequence" refers to a sequence capable of specifically hybridizing to a target sequence. The antisense sequence may include DNA, RNA, or any nucleic acid mimic or analog such as peptide nucleic acid (PNA); oligonucleotides having modified backbone linkages such as phosphorothioates, methylphosphonates, or benzylphosphonates; oligonucleotides having modified sugar groups such as 2'-methoxyethyl sugars or 2'-methoxyethoxy sugars; or oligonucleotides having modified bases such as 5-methyl cytosine, 2'-deoxyuracil, or 7-deaza-2'-deoxyguanosine.

"Antisense technology" refers to any technology which relies on the specific hybridization of an antisense sequence to a target sequence.

A "bin" is a portion of computer memory space used by a computer program for storage of data, and bounded in such a manner that data stored in a bin may be retrieved by the program.

"Biologically active" refers to an amino acid sequence having a structural, regulatory, or biochemical function of a naturally occurring amino acid sequence.

"Clone joining" is a process for combining gene bins based upon the bins' containing sequence information from the same clone. The sequences may assemble into a primary gene transcript as well as one or more splice variants.

"Complementary" describes the relationship between two single-stranded nucleic acid sequences that anneal by base-pairing (5'-A-G-T-3' pairs with its complement 3'-T-C-A-5').

A "component sequence" is a nucleic acid sequence selected by a computer program such as PHRED and used to assemble a consensus or template sequence from one or more component sequences.

A "consensus sequence" or "template sequence" is a nucleic acid sequence which has been assembled from overlapping sequences, using a computer program for fragment assembly such as the GELVIEW fragment assembly system (Genetics Computer Group (GCG), Madison WI) or using a relational database management system (RDMS).

"Conservative amino acid substitutions" are those substitutions that, when made, least interfere with the properties of the original protein, i.e., the structure and especially the function of the protein is conserved and not significantly changed by such substitutions. The table below shows amino acids which may be substituted for an original amino acid in a protein and which are regarded as conservative substitutions.

Original Residue	Conservative Substitution
Ala	Gly, Ser
Arg	His, Lys
Asn	Asp, Gln, His
Asp	Asn, Glu
Cys	Ala, Ser
Gln	Asn, Glu, His
Glu	Asp, Gln, His
Gly	Ala
His	Asn, Arg, Gln, Glu
Ile	Leu, Val
Leu	Ile, Val
Lys	Arg, Gln, Glu
Met	Leu, Ile
Phe	His, Met, Leu, Trp, Tyr
Ser	Cys, Thr
Thr	Ser, Val
Trp	Phe, Tyr
Tyr	His, Phe, Trp
Val	Ile, Leu, Thr

Conservative substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a beta sheet or alpha helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain.

"Deletion" refers to a change in either a nucleic or amino acid sequence in which at least one nucleotide or amino acid residue, respectively, is absent.

"Derivative" refers to the chemical modification of a nucleic acid sequence, such as by replacement of hydrogen by an alkyl, acyl, amino, hydroxyl, or other group.

"Differential expression" refers to increased or upregulated; or decreased, downregulated, or absent gene or protein expression, determined by comparing at least two different samples. Such comparisons may be carried out between, for example, a treated and an untreated sample, or a diseased and a normal sample.

The terms "element" and "array element" refer to a polynucleotide, polypeptide, or other chemical compound having a unique and defined position on a microarray.

The term "modulate" refers to a change in the activity of MDDT. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of MDDT.

"E-value" refers to the statistical probability that a match between two sequences occurred by chance.

"Exon shuffling" refers to the recombination of different coding regions (exons). Since an exon may represent a structural or functional domain of the encoded protein, new proteins may be assembled through the novel reassortment of stable substructures, thus allowing acceleration of the evolution of new protein functions.

A "fragment" is a unique portion of mddt or MDDT which is identical in sequence to but shorter in length than the parent sequence. A fragment may comprise up to the entire length of the defined sequence, minus one nucleotide/amino acid residue. For example, a fragment may comprise from 10 to 1000 contiguous amino acid residues or nucleotides. A fragment used as a probe, primer, antigen, therapeutic molecule, or for other purposes, may be at least 5, 10, 15, 16, 20, 25, 30, 40, 50, 60, 75, 100, 150, 250 or at least 500 contiguous amino acid residues or nucleotides in length. Fragments may be preferentially selected from certain regions of a molecule. For example, a polypeptide fragment may comprise a certain length of contiguous amino acids selected from the first 250 or 500 amino acids (or first 25% or 50%) of a polypeptide as shown in a certain defined sequence. Clearly these lengths are exemplary, and any length that is supported by the specification, including the Sequence Listing and the figures, may be encompassed by the present embodiments.

A fragment of mddt comprises a region of unique polynucleotide sequence that specifically identifies mddt, for example, as distinct from any other sequence in the same genome. A fragment of mddt is useful, for example, in hybridization and amplification technologies and in analogous methods that distinguish mddt from related polynucleotide sequences. The precise length of a fragment of mddt and the region of mddt to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A fragment of MDDT is encoded by a fragment of mddt. A fragment of MDDT comprises a region of unique amino acid sequence that specifically identifies MDDT. For example, a fragment of MDDT is useful as an immunogenic peptide for the development of antibodies that specifically

recognize MDDT. The precise length of a fragment of MDDT and the region of MDDT to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A "full length" nucleotide sequence is one containing at least a start site for translation to a protein sequence, followed by an open reading frame and a stop site, and encoding a "full length" polypeptide.

"Hit" refers to a sequence whose annotation will be used to describe a given template. Criteria for selecting the top hit are as follows: if the template has one or more exact nucleic acid matches, the top hit is the exact match with highest percent identity. If the template has no exact matches but has significant protein hits, the top hit is the protein hit with the lowest E-value. If the template has no significant protein hits, but does have significant non-exact nucleotide hits, the top hit is the nucleotide hit with the lowest E-value.

"Homology" refers to sequence similarity either between a reference nucleic acid sequence and at least a fragment of an mddt or between a reference amino acid sequence and a fragment of an MDDT.

"Hybridization" refers to the process by which a strand of nucleotides anneals with a complementary strand through base pairing. Specific hybridization is an indication that two nucleic acid sequences share a high degree of identity. Specific hybridization complexes form under defined annealing conditions, and remain hybridized after the "washing" step. The defined hybridization conditions include the annealing conditions and the washing step(s), the latter of which is particularly important in determining the stringency of the hybridization process, with more stringent conditions allowing less non-specific binding, i.e., binding between pairs of nucleic acid probes that are not perfectly matched. Permissive conditions for annealing of nucleic acid sequences are routinely determinable and may be consistent among hybridization experiments, whereas wash conditions may be varied among experiments to achieve the desired stringency.

Generally, stringency of hybridization is expressed with reference to the temperature under which the wash step is carried out. Generally, such wash temperatures are selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. An equation for calculating T_m and conditions for nucleic acid hybridization is well known and can be found in Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; specifically see volume 2, chapter 9.

High stringency conditions for hybridization between polynucleotides of the present invention include wash conditions of 68°C in the presence of about 0.2 x SSC and about 0.1% SDS,

for 1 hour. Alternatively, temperatures of about 65°C, 60°C, or 55°C may be used. SSC concentration may be varied from about 0.2 to 2 x SSC, with SDS being present at about 0.1%. Typically, blocking reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, denatured salmon sperm DNA at about 100-200 μg/ml. Useful variations on these conditions will be readily apparent to those skilled in the art. Hybridization, particularly under high stringency conditions, may be suggestive of evolutionary similarity between the nucleotides. Such similarity is strongly indicative of a similar role for the nucleotides and their resultant proteins.

Other parameters, such as temperature, salt concentration, and detergent concentration may be varied to achieve the desired stringency. Denaturants, such as formamide at a concentration of about 35-50% v/v, may also be used under particular circumstances, such as RNA:DNA hybridizations. Appropriate hybridization conditions are routinely determinable by one of ordinary skill in the art.

"Immunologically active" or "immunogenic" describes the potential for a natural, recombinant, or synthetic peptide, epitope, polypeptide, or protein to induce antibody production in appropriate animals, cells, or cell lines.

"Immune response" can refer to conditions associated with inflammation, trauma, immune disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

An "immunogenic fragment" is a polypeptide or oligopeptide fragment of MDDT which is capable of eliciting an immune response when introduced into a living organism, for example, a mammal. The term "immunogenic fragment" also includes any polypeptide or oligopeptide fragment of MDDT which can be useful in any of the antibody production methods disclosed herein or known in the art.

"Insertion" or "addition" refers to a change in either a nucleic or amino acid sequence in which at least one nucleotide or residue, respectively, is added to the sequence.

"Labeling" refers to the covalent or noncovalent joining of a polynucleotide, polypeptide, or antibody with a reporter molecule capable of producing a detectable or measurable signal.

"Microarray" is any arrangement of nucleic acids, amino acids, antibodies, etc., on a substrate. The substrate may be a solid support such as beads, glass, paper, nitrocellulose, nylon, or an appropriate membrane.

"Linkers" are short stretches of nucleotide sequence which may be added to a vector or an mddt to create restriction endonuclease sites to facilitate cloning. "Polylinkers" are engineered to incorporate multiple restriction enzyme sites and to provide for the use of enzymes which leave 5' or 3' overhangs (e.g., BamHI, EcoRI, and HindIII) and those which provide blunt ends (e.g., EcoRV,

SnaBI, and StuI).

"Naturally occurring" refers to an endogenous polynucleotide or polypeptide that may be isolated from viruses or prokaryotic or eukaryotic cells.

"Nucleic acid sequence" refers to the specific order of nucleotides joined by phosphodiester bonds in a linear, polymeric arrangement. Depending on the number of nucleotides, the nucleic acid sequence can be considered an oligomer, oligonucleotide, or polynucleotide. The nucleic acid can be DNA, RNA, or any nucleic acid analog, such as PNA, may be of genomic or synthetic origin, may be either double-stranded or single-stranded, and can represent either the sense or antisense (complementary) strand.

"Oligomer" refers to a nucleic acid sequence of at least about 6 nucleotides and as many as about 60 nucleotides, preferably about 15 to 40 nucleotides, and most preferably between about 20 and 30 nucleotides, that may be used in hybridization or amplification technologies. Oligomers may be used as, e.g., primers for PCR, and are usually chemically synthesized.

"Operably linked" refers to the situation in which a first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Generally, operably linked DNA sequences may be in close proximity or contiguous and, where necessary to join two protein coding regions, in the same reading frame.

"Peptide nucleic acid" (PNA) refers to a DNA mimic in which nucleotide bases are attached to a pseudopeptide backbone to increase stability. PNAs, also designated antigene agents, can prevent gene expression by targeting complementary messenger RNA.

The phrases "percent identity" and "% identity", as applied to polynucleotide sequences, refer to the percentage of residue matches between at least two polynucleotide sequences aligned using a standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way, gaps in the sequences being compared in order to optimize alignment between two sequences, and therefore achieve a more meaningful comparison of the two sequences.

Percent identity between polynucleotide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program. This program is part of the LASERGENE software package, a suite of molecular biological analysis programs (DNASTAR, Madison WI). CLUSTAL V is described in Higgins, D.G. and Sharp, P.M. (1989) CABIOS 5:151-153 and in Higgins, D.G. et al. (1992) CABIOS 8:189-191. For pairwise alignments of polynucleotide sequences, the default parameters are set as follows: Ktuple=2, gap penalty=5, window=4, and "diagonals saved"=4. The "weighted" residue weight table is selected as the default. Percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polynucleotide sequence pairs.

Alternatively, a suite of commonly used and freely available sequence comparison algorithms can be used that are provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at http://www.ncbi.nlm.nih.gov/BLAST/. The BLAST software suite includes various sequence analysis programs including "BLASTN," that is used to determine alignment between a known polynucleotide sequence and other sequences on a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at http://www.ncbi.nlm.nih.gov/gorf/bl2/. The "BLAST 2 Sequences" tool can be used for both BLASTN and BLASTP (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use BLASTN with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62
Reward for match: 1
Penalty for mismatch: -2
Open Gap: 5 and Extension Gap: 2 penalties
Gap x drop-off: 50
Expect: 10
Word Size: 11
Filter: on

Percent identity may be measured over the length of an entire defined sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined sequence, for instance, a fragment of at least 20, at least 30, at least 40, at least 50, at least 70, at least 100, or at least 200 contiguous nucleotides. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in figures or Sequence Listings, may be used to describe a length over which percentage identity may be measured.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences due to the degeneracy of the genetic code. It is understood that changes in nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that all encode substantially the same protein.

The phrases "percent identity" and "% identity", as applied to polypeptide sequences, refer to the percentage of residue matches between at least two polypeptide sequences aligned using a

standardized algorithm. Methods of polypeptide sequence alignment are well-known. Some alignment methods take into account conservative amino acid substitutions. Such conservative substitutions, explained in more detail above, generally preserve the hydrophobicity and acidity of the substituted residue, thus preserving the structure (and therefore function) of the folded polypeptide.

Percent identity between polypeptide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program (described and referenced above). For pairwise alignments of polypeptide sequences using CLUSTAL V, the default parameters are set as follows: Ktuple=1, gap penalty=3, window=5, and "diagonals saved"=5. The PAM250 matrix is selected as the default residue weight table. As with polynucleotide alignments, the percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polypeptide sequence pairs.

Alternatively the NCBI BLAST software suite may be used. For example, for a pairwise comparison of two polypeptide sequences, one may use the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) with BLASTP set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Open Gap: 11 and Extension Gap: 1 penalty

Gap x drop-off: 50

Expect: 10

Word Size: 3

Filter: on

Percent identity may be measured over the length of an entire defined polypeptide sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance, a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in figures or Sequence Listings, may be used to describe a length over which percentage identity may be measured.

"Post-translational modification" of an MDDT may involve lipidation, glycosylation, phosphorylation, acetylation, racemization, proteolytic cleavage, and other modifications known in the art. These processes may occur synthetically or biochemically. Biochemical modifications will vary by cell type depending on the enzymatic milieu and the MDDT.

"Probe" refers to mddt or fragments thereof, which are used to detect identical, allelic or related nucleic acid sequences. Probes are isolated oligonucleotides or polynucleotides attached to a detectable label or reporter molecule. Typical labels include radioactive isotopes, ligands,

chemiluminescent agents, and enzymes. "Primers" are short nucleic acids, usually DNA oligonucleotides, which may be annealed to a target polynucleotide by complementary base-pairing. The primer may then be extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification (and identification) of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR).

Probes and primers as used in the present invention typically comprise at least 15 contiguous nucleotides of a known sequence. In order to enhance specificity, longer probes and primers may also be employed, such as probes and primers that comprise at least 20, 30, 40, 50, 60, 70, 80, 90, 100, or at least 150 consecutive nucleotides of the disclosed nucleic acid sequences. Probes and primers may be considerably longer than these examples, and it is understood that any length supported by the specification, including the figures and Sequence Listing, may be used.

Methods for preparing and using probes and primers are described in the references, for example Sambrook, J. et al., (1989, Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY); Ausubel, F.M. et al., (1999, Short Protocols in Molecular Biology, 4th ed. Greene Publ. John Wiley & Sons Assoc. & Wiley-Interesciences, New York NY); and Innis, M. et al., (1990; PCR Protocols, A Guide to Methods and Applications, Academic Press, San Diego CA). PCR primer pairs can be derived from a known sequence, for example, by using computer programs intended for that purpose such as Primer (Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge MA).

Oligonucleotides for use as primers are selected using software known in the art for such purpose. For example, OLIGO 4.06 software is useful for the selection of PCR primer pairs of up to 100 nucleotides each, and for the analysis of oligonucleotides and larger polynucleotides of up to 5,000 nucleotides from an input polynucleotide sequence of up to 32 kilobases. Similar primer selection programs have incorporated additional features for expanded capabilities. For example, the PrimOU primer selection program (available to the public from the Genome Center at University of Texas South West Medical Center, Dallas TX) is capable of choosing specific primers from megabase sequences and is thus useful for designing primers on a genome-wide scope. The Primer3 primer selection program (available to the public from the Whitehead Institute/MIT Center for Genome Research, Cambridge MA) allows the user to input a "mispriming library," in which sequences to avoid as primer binding sites are user-specified. Primer3 is useful, in particular, for the selection of oligonucleotides for microarrays. (The source code for the latter two primer selection programs may also be obtained from their respective sources and modified to meet the user's specific needs.) The PrimeGen program (available to the public from the UK Human Genome Mapping Project Resource Centre, Cambridge UK) designs primers based on multiple sequence alignments, thereby allowing selection of primers that hybridize to either the most conserved or least conserved

regions of aligned nucleic acid sequences. Hence, this program is useful for identification of both unique and conserved oligonucleotides and polynucleotide fragments. The oligonucleotides and polynucleotide fragments identified by any of the above selection methods are useful in hybridization technologies, for example, as PCR or sequencing primers, microarray elements, or specific probes to identify fully or partially complementary polynucleotides in a sample of nucleic acids. Methods of oligonucleotide selection are not limited to those described above.

"Purified" refers to molecules, either polynucleotides or polypeptides that are isolated or separated from their natural environment and are at least 60% free, preferably at least 75% free, and most preferably at least 90% free from other compounds with which they are naturally associated.

A "recombinant nucleic acid" is a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two or more otherwise separated segments of sequence. This artificial combination is often accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques such as those described in Sambrook, supra. The term recombinant includes nucleic acids that have been altered solely by addition, substitution, or deletion of a portion of the nucleic acid. Frequently, a recombinant nucleic acid may include a nucleic acid sequence operably linked to a promoter sequence. Such a recombinant nucleic acid may be part of a vector that is used, for example, to transform a cell.

Alternatively, such recombinant nucleic acids may be part of a viral vector, e.g., based on a vaccinia virus, that could be use to vaccinate a mammal wherein the recombinant nucleic acid is expressed, inducing a protective immunological response in the mammal.

"Regulatory element" refers to a nucleic acid sequence from nontranslated regions of a gene, and includes enhancers, promoters, introns, and 3' untranslated regions, which interact with host proteins to carry out or regulate transcription or translation.

"Reporter" molecules are chemical or biochemical moieties used for labeling a nucleic acid, an amino acid, or an antibody. They include radionuclides; enzymes; fluorescent, chemiluminescent, or chromogenic agents; substrates; cofactors; inhibitors; magnetic particles; and other moieties known in the art.

An "RNA equivalent," in reference to a DNA sequence, is composed of the same linear sequence of nucleotides as the reference DNA sequence with the exception that all occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

"Sample" is used in its broadest sense. Samples may contain nucleic or amino acids, antibodies, or other materials, and may be derived from any source (e.g., bodily fluids including, but not limited to, saliva, blood, and urine; chromosome(s), organelles, or membranes isolated from a

cell; genomic DNA, RNA, or cDNA in solution or bound to a substrate; and cleared cells or tissues or blots or imprints from such cells or tissues).

"Specific binding" or "specifically binding" refers to the interaction between a protein or peptide and its agonist, antibody, antagonist, or other binding partner. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide containing epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

"Substitution" refers to the replacement of at least one nucleotide or amino acid by a different nucleotide or amino acid.

"Substrate" refers to any suitable rigid or semi-rigid support including, e.g., membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles or capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

A "transcript image" or "expression profile" refers to the collective pattern of gene expression by a particular cell type or tissue under given conditions at a given time.

"Transformation" refers to a process by which exogenous DNA enters a recipient cell. Transformation may occur under natural or artificial conditions using various methods well known in the art. Transformation may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method is selected based on the host cell being transformed.

"Transformants" include stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as cells which transiently express inserted DNA or RNA.

A "transgenic organism," as used herein, is any organism, including but not limited to animals and plants, in which one or more of the cells of the organism contains heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or in vitro fertilization, but rather is directed to the introduction of a recombinant DNA molecule. The transgenic organisms contemplated in accordance with the present invention include bacteria, cyanobacteria, fungi, and plants and animals. The isolated DNA of the present invention can be introduced into the host by methods known in the art, for example infection, transfection,

transformation or transconjugation. Techniques for transferring the DNA of the present invention into such organisms are widely known and provided in references such as Sambrook et al. (1989), supra.

A "variant" of a particular nucleic acid sequence is defined as a nucleic acid sequence having at least 25% sequence identity to the particular nucleic acid sequence over a certain length of one of the nucleic acid sequences using BLASTN with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of nucleic acids may show, for example, at least 30%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a certain defined length. The variant may result in "conservative" amino acid changes which do not affect structural and/or chemical properties. A variant may be described as, for example, an "allelic" (as defined above), "splice," "species," or "polymorphic" variant. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternate splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or lack domains that are present in the reference molecule. Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides generally will have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

In an alternative, variants of the polynucleotides of the present invention may be generated through recombinant methods. One possible method is a DNA shuffling technique such as MOLECULARBREEDING (Maxygen Inc., Santa Clara CA; described in U.S. Patent Number 5,837,458; Chang, C.-C. et al. (1999) Nat. Biotechnol. 17:793-797; Christians, F.C. et al. (1999) Nat. Biotechnol. 17:259-264; and Crameri, A. et al. (1996) Nat. Biotechnol. 14:315-319) to alter or improve the biological properties of MDDT, such as its biological or enzymatic activity or its ability to bind to other molecules or compounds. DNA shuffling is a process by which a library of gene variants is produced using PCR-mediated recombination of gene fragments. The library is then subjected to selection or screening procedures that identify those gene variants with the desired properties. These preferred variants may then be pooled and further subjected to recursive rounds of DNA shuffling and selection/screening. Thus, genetic diversity is created through "artificial" breeding and rapid molecular evolution. For example, fragments of a single gene containing random point mutations may be recombined, screened, and then reshuffled until the desired properties are

optimized. Alternatively, fragments of a given gene may be recombined with fragments of homologous genes in the same gene family, either from the same or different species, thereby maximizing the genetic diversity of multiple naturally occurring genes in a directed and controllable manner.

A "variant" of a particular polypeptide sequence is defined as a polypeptide sequence having at least 40% sequence identity to the particular polypeptide sequence over a certain length of one of the polypeptide sequences using BLASTP with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of polypeptides may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a certain defined length of one of the polypeptides.

THE INVENTION

In a particular embodiment, cDNA sequences derived from human tissues and cell lines were aligned based on nucleotide sequence identity and assembled into "consensus" or "template" sequences which are designated by the template identification numbers (template IDs) in column 2 of Table 2. The sequence identification numbers (SEQ ID NO:s) corresponding to the template IDs are shown in column 1. The template sequences have similarity to GenBank sequences, or "hits," as designated by the GI Numbers in column 3. The statistical probability of each GenBank hit is indicated by a probability score in column 4, and the functional annotation corresponding to each GenBank hit is listed in column 5.

The invention incorporates the nucleic acid sequences of these templates as disclosed in the Sequence Listing and the use of these sequences in the diagnosis and treatment of disease states characterized by defects in disease detection and treatment molecules. The invention further utilizes these sequences in hybridization and amplification technologies, and in particular, in technologies which assess gene expression patterns correlated with specific cells or tissues and their responses <u>in vivo</u> or <u>in vitro</u> to pharmaceutical agents, toxins, and other treatments. In this manner, the sequences of the present invention are used to develop a transcript image for a particular cell or tissue.

<u>Derivation of Nucleic Acid Sequences</u>

cDNA was isolated from libraries constructed using RNA derived from normal and diseased human tissues and cell lines. The human tissues and cell lines used for cDNA library construction were selected from a broad range of sources to provide a diverse population of cDNAs representative of gene transcription throughout the human body. Descriptions of the human tissues and cell lines used for cDNA library construction are provided in the LIFESEQ database (Incyte Genomics, Inc.

(Incyte), Palo Alto CA). Human tissues were broadly selected from, for example, cardiovascular, dermatologic, endocrine, gastrointestinal, hematopoietic/immune system, musculoskeletal, neural, reproductive, and urologic sources.

Cell lines used for cDNA library construction were derived from, for example, leukemic cells, teratocarcinomas, neuroepitheliomas, cervical carcinoma, lung fibroblasts, and endothelial cells. Such cell lines include, for example, THP-1, Jurkat, HUVEC, hNT2, WI38, HeLa, and other cell lines commonly used and available from public depositories (American Type Culture Collection, Manassas VA). Prior to mRNA isolation, cell lines were untreated, treated with a pharmaceutical agent such as 5'-aza-2'-deoxycytidine, treated with an activating agent such as lipopolysaccharide in the case of leukocytic cell lines, or, in the case of endothelial cell lines, subjected to shear stress.

Sequencing of the cDNAs

Methods for DNA sequencing are well known in the art. Conventional enzymatic methods employ the Klenow fragment of DNA polymerase I, SEQUENASE DNA polymerase (U.S. Biochemical Corporation, Cleveland OH), Taq polymerase (Applied Biosystems, Foster City CA), thermostable T7 polymerase (Amersham Pharmacia Biotech, Inc. (Amersham Pharmacia Biotech), Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies Inc. (Life Technologies), Gaithersburg MD), to extend the nucleic acid sequence from an oligonucleotide primer annealed to the DNA template of interest. Methods have been developed for the use of both single-stranded and double-stranded templates. Chain termination reaction products may be electrophoresed on urea-polyacrylamide gels and detected either by autoradiography (for radioisotope-labeled nucleotides) or by fluorescence (for fluorophore-labeled nucleotides). Automated methods for mechanized reaction preparation, sequencing, and analysis using fluorescence detection methods have been developed. Machines used to prepare cDNAs for sequencing can include the MICROLAB 2200 liquid transfer system (Hamilton Company (Hamilton), Reno NV), Peltier thermal cycler (PTC200; MJ Research, Inc. (MJ Research), Watertown MA), and ABI CATALYST 800 thermal cycler (Applied Biosystems). Sequencing can be carried out using, for example, the ABI 373 or 377 (Applied Biosystems) or MEGABACE 1000 (Molecular Dynamics, Inc. (Molecular Dynamics), Sunnyvale CA) DNA sequencing systems, or other automated and manual sequencing systems well known in the art.

The nucleotide sequences of the Sequence Listing have been prepared by current, state-of-the-art, automated methods and, as such, may contain occasional sequencing errors or unidentified nucleotides. Such unidentified nucleotides are designated by an N. These infrequent unidentified bases do not represent a hindrance to practicing the invention for those skilled in the art. Several

methods employing standard recombinant techniques may be used to correct errors and complete the missing sequence information. (See, e.g., those described in Ausubel, F.M. et al. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY; and Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY.)

Assembly of cDNA Sequences

Human polynucleotide sequences may be assembled using programs or algorithms well known in the art. Sequences to be assembled are related, wholly or in part, and may be derived from a single or many different transcripts. Assembly of the sequences can be performed using such programs as PHRAP (Phils Revised Assembly Program) and the GELVIEW fragment assembly system (GCG), or other methods known in the art.

Alternatively, cDNA sequences are used as "component" sequences that are assembled into "template" or "consensus" sequences as follows. Sequence chromatograms are processed, verified, and quality scores are obtained using PHRED. Raw sequences are edited using an editing pathway known as Block 1 (See, e.g., the LIFESEQ Assembled User Guide, Incyte Genomics, Palo Alto, CA). A series of BLAST comparisons is performed and low-information segments and repetitive elements (e.g., dinucleotide repeats, Alu repeats, etc.) are replaced by "n's", or masked, to prevent spurious matches. Mitochondrial and ribosomal RNA sequences are also removed. The processed sequences are then loaded into a relational database management system (RDMS) which assigns edited sequences to existing templates, if available. When additional sequences are added into the RDMS, a process is initiated which modifies existing templates or creates new templates from works in progress (i.e., nonfinal assembled sequences) containing queued sequences or the sequences themselves. After the new sequences have been assigned to templates, the templates can be merged into bins. If multiple templates exist in one bin, the bin can be split and the templates reannotated.

Once gene bins have been generated based upon sequence alignments, bins are "clone joined" based upon clone information. Clone joining occurs when the 5' sequence of one clone is present in one bin and the 3' sequence from the same clone is present in a different bin, indicating that the two bins should be merged into a single bin. Only bins which share at least two different clones are merged.

A resultant template sequence may contain either a partial or a full length open reading frame, or all or part of a genetic regulatory element. This variation is due in part to the fact that the full length cDNAs of many genes are several hundred, and sometimes several thousand, bases in length. With current technology, cDNAs comprising the coding regions of large genes cannot be cloned because of vector limitations, incomplete reverse transcription of the mRNA, or incomplete "second strand" synthesis. Template sequences may be extended to include additional contiguous

sequences derived from the parent RNA transcript using a variety of methods known to those of skill in the art. Extension may thus be used to achieve the full length coding sequence of a gene.

Analysis of the cDNA Sequences

The cDNA sequences are analyzed using a variety of programs and algorithms which are well known in the art. (See, e.g., Ausubel, 1997, supra, Chapter 7.7; Meyers, R.A. (Ed.) (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853; and Table 8.) These analyses comprise both reading frame determinations, e.g., based on triplet codon periodicity for particular organisms (Fickett, J.W. (1982) Nucleic Acids Res. 10:5303-5318); analyses of potential start and stop codons; and homology searches.

Computer programs known to those of skill in the art for performing computer-assisted searches for amino acid and nucleic acid sequence similarity, include, for example, Basic Local Alignment Search Tool (BLAST; Altschul, S.F. (1993) J. Mol. Evol. 36:290-300; Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410). BLAST is especially useful in determining exact matches and comparing two sequence fragments of arbitrary but equal lengths, whose alignment is locally maximal and for which the alignment score meets or exceeds a threshold or cutoff score set by the user (Karlin, S. et al. (1988) Proc. Natl. Acad. Sci. USA 85:841-845). Using an appropriate search tool (e.g., BLAST or HMM), GenBank, SwissProt, BLOCKS, PFAM and other databases may be searched for sequences containing regions of homology to a query mddt or MDDT of the present invention.

Other approaches to the identification, assembly, storage, and display of nucleotide and polypeptide sequences are provided in "Relational Database for Storing Biomolecule Information," U.S.S.N. 08/947,845, filed October 9, 1997; "Project-Based Full-Length Biomolecular Sequence Database," U.S. Patent Number 5,953,727; and "Relational Database and System for Storing Information Relating to Biomolecular Sequences," U.S.S.N. 09/034,807, filed March 4, 1998, all of which are incorporated by reference herein in their entirety.

Protein hierarchies can be assigned to the putative encoded polypeptide based on, e.g., motif, BLAST, or biological analysis. Methods for assigning these hierarchies are described, for example, in "Database System Employing Protein Function Hierarchies for Viewing Biomolecular Sequence Data," U.S. Patent Number 6,023,659, incorporated herein by reference.

Human Disease Detection and Treatment Molecule Sequences

The mddt of the present invention may be used for a variety of diagnostic and therapeutic purposes. For example, an mddt may be used to diagnose a particular condition, disease, or disorder associated with disease detection and treatment molecules. Such conditions, diseases, and disorders

include, but are not limited to, a cell proliferative disorder, such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, a cancer of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; and an autoimmune/inflammatory disorder, such as actinic keratosis, acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, arteriosclerosis, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, bronchitis, bursitis, cholecystitis, cirrhosis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, paroxysmal nocturnal hemoglobinuria, hepatitis, hypereosinophilia, irritable bowel syndrome, episodic lymphopenia with lymphocytotoxins, mixed connective tissue disease (MCTD), multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, myelofibrosis, osteoarthritis, osteoporosis, pancreatitis, polycythemia vera, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, primary thrombocythemia, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, trauma, and hematopoietic cancer including lymphoma, leukemia, and myeloma. The mddt can be used to detect the presence of, or to quantify the amount of, an mddt-related polynucleotide in a sample. This information is then compared to information obtained from appropriate reference samples, and a diagnosis is established. Alternatively, a polynucleotide complementary to a given mddt can inhibit or inactivate a therapeutically relevant gene related to the mddt.

Analysis of mddt Expression Patterns

The expression of mddt may be routinely assessed by hybridization-based methods to determine, for example, the tissue-specificity, disease-specificity, or developmental stage-specificity of mddt expression. For example, the level of expression of mddt may be compared among different cell types or tissues, among diseased and normal cell types or tissues, among cell types or tissues at different developmental stages, or among cell types or tissues undergoing various treatments. This type of analysis is useful, for example, to assess the relative levels of mddt expression in fully or partially differentiated cells or tissues, to determine if changes in mddt expression levels are

correlated with the development or progression of specific disease states, and to assess the response of a cell or tissue to a specific therapy, for example, in pharmacological or toxicological studies. Methods for the analysis of mddt expression are based on hybridization and amplification technologies and include membrane-based procedures such as northern blot analysis, high-throughput procedures that utilize, for example, microarrays, and PCR-based procedures.

Hybridization and Genetic Analysis

The mddt, their fragments, or complementary sequences, may be used to identify the presence of and/or to determine the degree of similarity between two (or more) nucleic acid sequences. The mddt may be hybridized to naturally occurring or recombinant nucleic acid sequences under appropriately selected temperatures and salt concentrations. Hybridization with a probe based on the nucleic acid sequence of at least one of the mddt allows for the detection of nucleic acid sequences, including genomic sequences, which are identical or related to the mddt of the Sequence Listing. Probes may be selected from non-conserved or unique regions of at least one of the polynucleotides of SEQ ID NO:1-104 and tested for their ability to identify or amplify the target nucleic acid sequence using standard protocols.

Polynucleotide sequences that are capable of hybridizing, in particular, to those shown in SEQ ID NO:1-104 and fragments thereof, can be identified using various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) Methods Enzymol. 152:399-407; Kimmel, A.R. (1987) Methods Enzymol. 152:507-511.) Hybridization conditions are discussed in "Definitions."

A probe for use in Southern or northern hybridization may be derived from a fragment of an mddt sequence, or its complement, that is up to several hundred nucleotides in length and is either single-stranded or double-stranded. Such probes may be hybridized in solution to biological materials such as plasmids, bacterial, yeast, or human artificial chromosomes, cleared or sectioned tissues, or to artificial substrates containing mddt. Microarrays are particularly suitable for identifying the presence of and detecting the level of expression for multiple genes of interest by examining gene expression correlated with, e.g., various stages of development, treatment with a drug or compound, or disease progression. An array analogous to a dot or slot blot may be used to arrange and link polynucleotides to the surface of a substrate using one or more of the following: mechanical (vacuum), chemical, thermal, or UV bonding procedures. Such an array may contain any number of mddt and may be produced by hand or by using available devices, materials, and machines.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci. USA 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. USA 94:2150-

2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.)

Probes may be labeled by either PCR or enzymatic techniques using a variety of commercially available reporter molecules. For example, commercial kits are available for radioactive and chemiluminescent labeling (Amersham Pharmacia Biotech) and for alkaline phosphatase labeling (Life Technologies). Alternatively, mddt may be cloned into commercially available vectors for the production of RNA probes. Such probes may be transcribed in the presence of at least one labeled nucleotide (e.g., ^{32}P-ATP, Amersham Pharmacia Biotech).

Additionally the polynucleotides of SEQ ID NO:1-104 or suitable fragments thereof can be used to isolate full length cDNA sequences utilizing hybridization and/or amplification procedures well known in the art, e.g., cDNA library screening, PCR amplification, etc. The molecular cloning of such full length cDNA sequences may employ the method of cDNA library screening with probes using the hybridization, stringency, washing, and probing strategies described above and in Ausubel, supra, Chapters 3, 5, and 6. These procedures may also be employed with genomic libraries to isolate genomic sequences of mddt in order to analyze, e.g., regulatory elements.

Genetic Mapping

Gene identification and mapping are important in the investigation and treatment of almost all conditions, diseases, and disorders. Cancer, cardiovascular disease, Alzheimer's disease, arthritis, diabetes, and mental illnesses are of particular interest. Each of these conditions is more complex than the single gene defects of sickle cell anemia or cystic fibrosis, with select groups of genes being predictive of predisposition for a particular condition, disease, or disorder. For example, cardiovascular disease may result from malfunctioning receptor molecules that fail to clear cholesterol from the bloodstream, and diabetes may result when a particular individual's immune system is activated by an infection and attacks the insulin-producing cells of the pancreas. In some studies, Alzheimer's disease has been linked to a gene on chromosome 21; other studies predict a different gene and location. Mapping of disease genes is a complex and reiterative process and generally proceeds from genetic linkage analysis to physical mapping.

As a condition is noted among members of a family, a genetic linkage map traces parts of chromosomes that are inherited in the same pattern as the condition. Statistics link the inheritance of particular conditions to particular regions of chromosomes, as defined by RFLP or other markers. (See, for example, Lander, E. S. and Botstein, D. (1986) Proc. Natl. Acad. Sci. USA 83:7353-7357.) Occasionally, genetic markers and their locations are known from previous studies. More often, however, the markers are simply stretches of DNA that differ among individuals. Examples of genetic linkage maps can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) World Wide Web site.

In another embodiment of the invention, mddt sequences may be used to generate hybridization probes useful in chromosomal mapping of naturally occurring genomic sequences. Either coding or noncoding sequences of mddt may be used, and in some instances, noncoding sequences may be preferable over coding sequences. For example, conservation of an mddt coding sequence among members of a multi-gene family may potentially cause undesired cross hybridization during chromosomal mapping. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355; Price, C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical chromosome mapping techniques and genetic map data. (See, e.g., Meyers, supra, pp. 965-968.) Correlation between the location of mddt on a physical chromosomal map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder. The mddt sequences may also be used to detect polymorphisms that are genetically linked to the inheritance of a particular condition, disease, or disorder.

In situ hybridization of chromosomal preparations and genetic mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending existing genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the number or arm of the corresponding human chromosome is not known. These new marker sequences can be mapped to human chromosomes and may provide valuable information to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once a disease or syndrome has been crudely correlated by genetic linkage with a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580.) The nucleotide sequences of the subject invention may also be used to detect differences in chromosomal architecture due to translocation, inversion, etc., among normal, carrier, or affected individuals.

Once a disease-associated gene is mapped to a chromosomal region, the gene must be cloned in order to identify mutations or other alterations (e.g., translocations or inversions) that may be correlated with disease. This process requires a physical map of the chromosomal region containing the disease-gene of interest along with associated markers. A physical map is necessary for determining the nucleotide sequence of and order of marker genes on a particular chromosomal region. Physical mapping techniques are well known in the art and require the generation of

overlapping sets of cloned DNA fragments from a particular organelle, chromosome, or genome. These clones are analyzed to reconstruct and catalog their order. Once the position of a marker is determined, the DNA from that region is obtained by consulting the catalog and selecting clones from that region. The gene of interest is located through positional cloning techniques using hybridization or similar methods.

Diagnostic Uses

The mddt of the present invention may be used to design probes useful in diagnostic assays. Such assays, well known to those skilled in the art, may be used to detect or confirm conditions, disorders, or diseases associated with abnormal levels of mddt expression. Labeled probes developed from mddt sequences are added to a sample under hybridizing conditions of desired stringency. In some instances, mddt, or fragments or oligonucleotides derived from mddt, may be used as primers in amplification steps prior to hybridization. The amount of hybridization complex formed is quantified and compared with standards for that cell or tissue. If mddt expression varies significantly from the standard, the assay indicates the presence of the condition, disorder, or disease. Qualitative or quantitative diagnostic methods may include northern, dot blot, or other membrane or dip-stick based technologies or multiple-sample format technologies such as PCR, enzyme-linked immunosorbent assay (ELISA)-like, pin, or chip-based assays.

The probes described above may also be used to monitor the progress of conditions, disorders, or diseases associated with abnormal levels of mddt expression, or to evaluate the efficacy of a particular therapeutic treatment. The candidate probe may be identified from the mddt that are specific to a given human tissue and have not been observed in GenBank or other genome databases. Such a probe may be used in animal studies, preclinical tests, clinical trials, or in monitoring the treatment of an individual patient. In a typical process, standard expression is established by methods well known in the art for use as a basis of comparison, samples from patients affected by the disorder or disease are combined with the probe to evaluate any deviation from the standard profile, and a therapeutic agent is administered and effects are monitored to generate a treatment profile. Efficacy is evaluated by determining whether the expression progresses toward or returns to the standard normal pattern. Treatment profiles may be generated over a period of several days or several months. Statistical methods well known to those skilled in the art may be use to determine the significance of such therapeutic agents.

The polynucleotides are also useful for identifying individuals from minute biological samples, for example, by matching the RFLP pattern of a sample's DNA to that of an individual's DNA. The polynucleotides of the present invention can also be used to determine the actual base-by-base DNA sequence of selected portions of an individual's genome. These sequences can be

used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, an individual can be identified through a unique set of DNA sequences. Once a unique ID database is established for an individual, positive identification of that individual can be made from extremely small tissue samples.

In a particular aspect, oligonucleotide primers derived from the mddt of the invention may be used to detect single nucleotide polymorphisms (SNPs). SNPs are substitutions, insertions and deletions that are a frequent cause of inherited or acquired genetic disease in humans. Methods of SNP detection include, but are not limited to, single-stranded conformation polymorphism (SSCP) and fluorescent SSCP (fSSCP) methods. In SSCP, oligonucleotide primers derived from mddt are used to amplify DNA using the polymerase chain reaction (PCR). The DNA may be derived, for example, from diseased or normal tissue, biopsy samples, bodily fluids, and the like. SNPs in the DNA cause differences in the secondary and tertiary structures of PCR products in single-stranded form, and these differences are detectable using gel electrophoresis in non-denaturing gels. In fSCCP, the oligonucleotide primers are fluorescently labeled, which allows detection of the amplimers in high-throughput equipment such as DNA sequencing machines. Additionally, sequence database analysis methods, termed in silico SNP (isSNP), are capable of identifying polymorphisms by comparing the sequences of individual overlapping DNA fragments which assemble into a common consensus sequence. These computer-based methods filter out sequence variations due to laboratory preparation of DNA and sequencing errors using statistical models and automated analyses of DNA sequence chromatograms. In the alternative, SNPs may be detected and characterized by mass spectrometry using, for example, the high throughput MASSARRAY system (Sequenom, Inc., San Diego CA).

DNA-based identification techniques are critical in forensic technology. DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, etc., can be amplified using, e.g., PCR, to identify individuals. (See, e.g., Erlich, H. (1992) PCR Technology, Freeman and Co., New York, NY). Similarly, polynucleotides of the present invention can be used as polymorphic markers.

There is also a need for reagents capable of identifying the source of a particular tissue. Appropriate reagents can comprise, for example, DNA probes or primers prepared from the sequences of the present invention that are specific for particular tissues. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

The polynucleotides of the present invention can also be used as molecular weight markers on nucleic acid gels or Southern blots, as diagnostic probes for the presence of a specific mRNA in a particular cell type, in the creation of subtracted cDNA libraries which aid in the discovery of novel

polynucleotides, in selection and synthesis of oligomers for attachment to an array or other support, and as an antigen to elicit an immune response.

Disease Model Systems Using mddt

The mddt of the invention or their mammalian homologs may be "knocked out" in an animal model system using homologous recombination in embryonic stem (ES) cells. Such techniques are well known in the art and are useful for the generation of animal models of human disease. (See, e.g., U.S. Patent Number 5,175,383 and U.S. Patent Number 5,767,337.) For example, mouse ES cells, such as the mouse 129/SvJ cell line, are derived from the early mouse embryo and grown in culture. The ES cells are transformed with a vector containing the gene of interest disrupted by a marker gene, e.g., the neomycin phosphotransferase gene (neo; Capecchi, M.R. (1989) Science 244:1288-1292). The vector integrates into the corresponding region of the host genome by homologous recombination. Alternatively, homologous recombination takes place using the Cre-loxP system to knockout a gene of interest in a tissue- or developmental stage-specific manner (Marth, J.D. (1996) Clin. Invest. 97:1999-2002; Wagner, K.U. et al. (1997) Nucleic Acids Res. 25:4323-4330). Transformed ES cells are identified and microinjected into mouse cell blastocysts such as those from the C57BL/6 mouse strain. The blastocysts are surgically transferred to pseudopregnant dams, and the resulting chimeric progeny are genotyped and bred to produce heterozygous or homozygous strains. Transgenic animals thus generated may be tested with potential therapeutic or toxic agents.

The mddt of the invention may also be manipulated in vitro in ES cells derived from human blastocysts. Human ES cells have the potential to differentiate into at least eight separate cell lineages including endoderm, mesoderm, and ectodermal cell types. These cell lineages differentiate into, for example, neural cells, hematopoietic lineages, and cardiomyocytes (Thomson, J.A. et al. (1998) Science 282:1145-1147).

The mddt of the invention can also be used to create "knockin" humanized animals (pigs) or transgenic animals (mice or rats) to model human disease. With knockin technology, a region of mddt is injected into animal ES cells, and the injected sequence integrates into the animal cell genome. Transformed cells are injected into blastulae, and the blastulae are implanted as described above. Transgenic progeny or inbred lines are studied and treated with potential pharmaceutical agents to obtain information on treatment of a human disease. Alternatively, a mammal inbred to overexpress mddt, resulting, e.g., in the secretion of MDDT in its milk, may also serve as a convenient source of that protein (Janne, J. et al. (1998) Biotechnol. Annu. Rev. 4:55-74).

Screening Assays

MDDT encoded by polynucleotides of the present invention may be used to screen for molecules that bind to or are bound by the encoded polypeptides. The binding of the polypeptide and

the molecule may activate (agonist), increase, inhibit (antagonist), or decrease activity of the polypeptide or the bound molecule. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a ligand or fragment thereof, a natural substrate, or a structural or functional mimetic. (See, Coligan et al., (1991) Current Protocols in Immunology 1(2): Chapter 5.) Similarly, the molecule can be closely related to the natural receptor to which the polypeptide binds, or to at least a fragment of the receptor, e.g., the active site. In either case, the molecule can be rationally designed using known techniques. Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, Drosophila, or E. coli. Cells expressing the polypeptide or cell membrane fractions which contain the expressed polypeptide are then contacted with a test compound and binding, stimulation, or inhibition of activity of either the polypeptide or the molecule is analyzed.

An assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a fluorophore, radioisotope, enzyme conjugate, or other detectable label. Alternatively, the assay may assess binding in the presence of a labeled competitor.

Additionally, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

Preferably, an ELISA assay using, e.g., a monoclonal or polyclonal antibody, can measure polypeptide level in a sample. The antibody can measure polypeptide level by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

All of the above assays can be used in a diagnostic or prognostic context. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptide from suitably manipulated cells or tissues.

Transcript Imaging and Toxicological Testing

Another embodiment relates to the use of mddt to develop a transcript image of a tissue or cell type. A transcript image represents the global pattern of gene expression by a particular tissue or cell type. Global gene expression patterns are analyzed by quantifying the number of expressed genes and their relative abundance under given conditions and at a given time. (See Seilhamer et al.,

"Comparative Gene Transcript Analysis," U.S. Patent Number 5,840,484, expressly incorporated by reference herein.) Thus a transcript image may be generated by hybridizing the polynucleotides of the present invention or their complements to the totality of transcripts or reverse transcripts of a particular tissue or cell type. In one embodiment, the hybridization takes place in high-throughput format, wherein the polynucleotides of the present invention or their complements comprise a subset of a plurality of elements on a microarray. The resultant transcript image would provide a profile of gene activity pertaining to disease detection and treatment molecules.

Transcript images which profile mddt expression may be generated using transcripts isolated from tissues, cell lines, biopsies, or other biological samples. The transcript image may thus reflect mddt expression in vivo, as in the case of a tissue or biopsy sample, or in vitro, as in the case of a cell line.

Transcript images which profile mddt expression may also be used in conjunction with in vitro model systems and preclinical evaluation of pharmaceuticals, as well as toxicological testing of industrial and naturally-occurring environmental compounds. All compounds induce characteristic gene expression patterns, frequently termed molecular fingerprints or toxicant signatures, which are indicative of mechanisms of action and toxicity (Nuwaysir, E. F. et al. (1999) Mol. Carcinog. 24:153-159; Steiner, S. and Anderson, N. L. (2000) Toxicol. Lett. 112-113:467-71, expressly incorporated by reference herein). If a test compound has a signature similar to that of a compound with known toxicity, it is likely to share those toxic properties. These fingerprints or signatures are most useful and refined when they contain expression information from a large number of genes and gene families. Ideally, a genome-wide measurement of expression provides the highest quality signature. Even genes whose expression is not altered by any tested compounds are important as well, as the levels of expression of these genes are used to normalize the rest of the expression data. The normalization procedure is useful for comparison of expression data after treatment with different compounds. While the assignment of gene function to elements of a toxicant signature aids in interpretation of toxicity mechanisms, knowledge of gene function is not necessary for the statistical matching of signatures which leads to prediction of toxicity. (See, for example, Press Release 00-02 from the National Institute of Environmental Health Sciences, released February 29, 2000, available at http://www.niehs.nih.gov/oc/news/toxchip.htm.) Therefore, it is important and desirable in toxicological screening using toxicant signatures to include all expressed gene sequences.

In one embodiment, the toxicity of a test compound is assessed by treating a biological sample containing nucleic acids with the test compound. Nucleic acids that are expressed in the treated biological sample are hybridized with one or more probes specific to the polynucleotides of the present invention, so that transcript levels corresponding to the polynucleotides of the present invention may be quantified. The transcript levels in the treated biological sample are compared with

levels in an untreated biological sample. Differences in the transcript levels between the two samples are indicative of a toxic response caused by the test compound in the treated sample.

Another particular embodiment relates to the use of MDDT encoded by polynucleotides of the present invention to analyze the proteome of a tissue or cell type. The term proteome refers to the global pattern of protein expression in a particular tissue or cell type. Each protein component of a proteome can be subjected individually to further analysis. Proteome expression patterns, or profiles, are analyzed by quantifying the number of expressed proteins and their relative abundance under given conditions and at a given time. A profile of a cell's proteome may thus be generated by separating and analyzing the polypeptides of a particular tissue or cell type. In one embodiment, the separation is achieved using two-dimensional gel electrophoresis, in which proteins from a sample are separated by isoelectric focusing in the first dimension, and then according to molecular weight by sodium dodecyl sulfate slab gel electrophoresis in the second dimension (Steiner and Anderson, supra). The proteins are visualized in the gel as discrete and uniquely positioned spots, typically by staining the gel with an agent such as Coomassie Blue or silver or fluorescent stains. The optical density of each protein spot is generally proportional to the level of the protein in the sample. The optical densities of equivalently positioned protein spots from different samples, for example, from biological samples either treated or untreated with a test compound or therapeutic agent, are compared to identify any changes in protein spot density related to the treatment. The proteins in the spots are partially sequenced using, for example, standard methods employing chemical or enzymatic cleavage followed by mass spectrometry. The identity of the protein in a spot may be determined by comparing its partial sequence, preferably of at least 5 contiguous amino acid residues, to the polypeptide sequences of the present invention. In some cases, further sequence data may be obtained for definitive protein identification.

A proteomic profile may also be generated using antibodies specific for MDDT to quantify the levels of MDDT expression. In one embodiment, the antibodies are used as elements on a microarray, and protein expression levels are quantified by exposing the microarray to the sample and detecting the levels of protein bound to each array element (Lueking, A. et al. (1999) Anal. Biochem. 270:103-11; Mendoze, L. G. et al. (1999) Biotechniques 27:778-88). Detection may be performed by a variety of methods known in the art, for example, by reacting the proteins in the sample with a thiol- or amino-reactive fluorescent compound and detecting the amount of fluorescence bound at each array element.

Toxicant signatures at the proteome level are also useful for toxicological screening, and should be analyzed in parallel with toxicant signatures at the transcript level. There is a poor correlation between transcript and protein abundances for some proteins in some tissues (Anderson, N. L. and Seilhamer, J. (1997) Electrophoresis 18:533-537), so proteome toxicant signatures may be

useful in the analysis of compounds which do not significantly affect the transcript image, but which alter the proteomic profile. In addition, the analysis of transcripts in body fluids is difficult, due to rapid degradation of mRNA, so proteomic profiling may be more reliable and informative in such cases.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins that are expressed in the treated biological sample are separated so that the amount of each protein can be quantified. The amount of each protein is compared to the amount of the corresponding protein in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample. Individual proteins are identified by sequencing the amino acid residues of the individual proteins and comparing these partial sequences to the MDDT encoded by polynucleotides of the present invention.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins from the biological sample are incubated with antibodies specific to the MDDT encoded by polynucleotides of the present invention. The amount of protein recognized by the antibodies is quantified. The amount of protein in the treated biological sample is compared with the amount in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample.

Transcript images may be used to profile mddt expression in distinct tissue types. This process can be used to determine disease detection and treatment molecule activity in a particular tissue type relative to this activity in a different tissue type. Transcript images may be used to generate a profile of mddt expression characteristic of diseased tissue. Transcript images of tissues before and after treatment may be used for diagnostic purposes, to monitor the progression of disease, and to monitor the efficacy of drug treatments for diseases which affect the activity of disease detection and treatment molecules.

Transcript images of cell lines can be used to assess disease detection and treatment molecule activity and/or to identify cell lines that lack or misregulate this activity. Such cell lines may then be treated with pharmaceutical agents, and a transcript image following treatment may indicate the efficacy of these agents in restoring desired levels of this activity. A similar approach may be used to assess the toxicity of pharmaceutical agents as reflected by undesirable changes in disease detection and treatment molecule activity. Candidate pharmaceutical agents may be evaluated by comparing their associated transcript images with those of pharmaceutical agents of known effectiveness.

<u>Antisense Molecules</u>

The polynucleotides of the present invention are useful in antisense technology. Antisense technology or therapy relies on the modulation of expression of a target protein through the specific binding of an antisense sequence to a target sequence encoding the target protein or directing its expression. (See, e.g., Agrawal, S., ed. (1996) Antisense Therapeutics, Humana Press Inc., Totawa NJ; Alama, A. et al. (1997) Pharmacol. Res. 36(3):171-178; Crooke, S.T. (1997) Adv. Pharmacol. 40:1-49; Sharma, H.W. and R. Narayanan (1995) Bioessays 17(12):1055-1063; and Lavrosky, Y. et al. (1997) Biochem. Mol. Med. 62(1):11-22.) An antisense sequence is a polynucleotide sequence capable of specifically hybridizing to at least a portion of the target sequence. Antisense sequences bind to cellular mRNA and/or genomic DNA, affecting translation and/or transcription. Antisense sequences can be DNA, RNA, or nucleic acid mimics and analogs. (See, e.g., Rossi, J.J. et al. (1991) Antisense Res. Dev. 1(3):285-288; Lee, R. et al. (1998) Biochemistry 37(3):900-1010; Pardridge, W.M. et al. (1995) Proc. Natl. Acad. Sci. USA 92(12):5592-5596; and Nielsen, P. E. and Haaima, G. (1997) Chem. Soc. Rev. 96:73-78.) Typically, the binding which results in modulation of expression occurs through hybridization or binding of complementary base pairs. Antisense sequences can also bind to DNA duplexes through specific interactions in the major groove of the double helix.

The polynucleotides of the present invention and fragments thereof can be used as antisense sequences to modify the expression of the polypeptide encoded by mddt. The antisense sequences can be produced ex vivo, such as by using any of the ABI nucleic acid synthesizer series (Applied Biosystems) or other automated systems known in the art. Antisense sequences can also be produced biologically, such as by transforming an appropriate host cell with an expression vector containing the sequence of interest. (See, e.g., Agrawal, supra.)

In therapeutic use, any gene delivery system suitable for introduction of the antisense sequences into appropriate target cells can be used. Antisense sequences can be delivered intracellularly in the form of an expression plasmid which, upon transcription, produces a sequence complementary to at least a portion of the cellular sequence encoding the target protein. (See, e.g., Slater, J.E., et al. (1998) J. Allergy Clin. Immunol. 102(3):469-475; and Scanlon, K.J., et al. (1995) 9(13):1288-1296.) Antisense sequences can also be introduced intracellularly through the use of viral vectors, such as retrovirus and adeno-associated virus vectors. (See, e.g., Miller, A.D. (1990) Blood 76:271; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New York NY; Uckert, W. and W. Walther (1994) Pharmacol. Ther. 63(3):323-347.) Other gene delivery mechanisms include liposome-derived systems, artificial viral envelopes, and other systems known in the art. (See, e.g., Rossi, J.J. (1995) Br. Med. Bull. 51(1):217-225; Boado, R.J. et al. (1998) J. Pharm. Sci. 87(11):1308-1315; and Morris, M.C. et al. (1997) Nucleic Acids Res. 25(14):2730-2736.)

Expression

In order to express a biologically active MDDT, the nucleotide sequences encoding MDDT or fragments thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding MDDT and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. (See, e.g., Sambrook, supra, Chapters 4, 8, 16, and 17; and Ausubel, supra, Chapters 9, 10, 13, and 16.)

A variety of expression vector/host systems may be utilized to contain and express sequences encoding MDDT. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal (mammalian) cell systems. (See, e.g., Sambrook, supra; Ausubel, 1995, supra, Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509; Bitter, G.A. et al. (1987) Methods Enzymol. 153:516-544; Scorer, C.A. et al. (1994) Bio/Technology 12:181-184; Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945; Takamatsu, N. (1987) EMBO J. 6:307-311; Coruzzi, G. et al. (1984) EMBO J. 3:1671-1680; Broglie, R. et al. (1984) Science 224:838-843; Winter, J. et al. (1991) Results Probl. Cell Differ. 17:85-105; The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196; Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659; and Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355.) Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. (See, e.g., Di Nicola, M. et al. (1998) Cancer Gen. Ther. 5(6):350-356; Yu, M. et al., (1993) Proc. Natl. Acad. Sci. USA 90(13):6340-6344; Buller, R.M. et al. (1985) Nature 317(6040):813-815; McGregor, D.P. et al. (1994) Mol. Immunol. 31(3):219-226; and Verma, I.M. and N. Somia (1997) Nature 389:239-242.) The invention is not limited by the host cell employed.

For long term production of recombinant proteins in mammalian systems, stable expression of MDDT in cell lines is preferred. For example, sequences encoding MDDT can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Any number of selection systems may be used to recover transformed cell lines. (See, e.g., Wigler,

M. et al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.; Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. USA 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14; Hartman, S.C. and R.C.Mulligan (1988) Proc. Natl. Acad. Sci. USA 85:8047-8051; Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131.)

Therapeutic Uses of mddt

The mddt of the invention may be used for somatic or germline gene therapy. Gene therapy may be performed to (i) correct a genetic deficiency (e.g., in the cases of severe combined immunodeficiency (SCID)-X1 disease characterized by X-linked inheritance (Cavazzana-Calvo, M. et al. (2000) Science 288:669-672), severe combined immunodeficiency syndrome associated with an inherited adenosine deaminase (ADA) deficiency (Blaese, R.M. et al. (1995) Science 270:475-480; Bordignon, C. et al. (1995) Science 270:470-475), cystic fibrosis (Zabner, J. et al. (1993) Cell 75:207-216; Crystal, R.G. et al. (1995) Hum. Gene Therapy 6:643-666; Crystal, R.G. et al. (1995) Hum. Gene Therapy 6:667-703), thalassemias, familial hypercholesterolemia, and hemophilia resulting from Factor VIII or Factor IX deficiencies (Crystal, R.G. (1995) Science 270:404-410; Verma, I.M. and Somia, N. (1997) Nature 389:239-242)), (ii) express a conditionally lethal gene product (e.g., in the case of cancers which result from unregulated cell proliferation), or (iii) express a protein which affords protection against intracellular parasites (e.g., against human retroviruses, such as human immunodeficiency virus (HIV) (Baltimore, D. (1988) Nature 335:395-396; Poeschla, E. et al. (1996) Proc. Natl. Acad. Sci. USA. 93:11395-11399), hepatitis B or C virus (HBV, HCV); fungal parasites, such as Candida albicans and Paracoccidioides brasiliensis; and protozoan parasites such as Plasmodium falciparum and Trypanosoma cruzi). In the case where a genetic deficiency in mddt expression or regulation causes disease, the expression of mddt from an appropriate population of transduced cells may alleviate the clinical manifestations caused by the genetic deficiency.

In a further embodiment of the invention, diseases or disorders caused by deficiencies in mddt are treated by constructing mammalian expression vectors comprising mddt and introducing these vectors by mechanical means into mddt-deficient cells. Mechanical transfer technologies for use with cells in vivo or ex vitro include (i) direct DNA microinjection into individual cells, (ii) ballistic gold particle delivery, (iii) liposome-mediated transfection, (iv) receptor-mediated gene transfer, and (v) the use of DNA transposons (Morgan, R.A. and Anderson, W.F. (1993) Annu. Rev. Biochem. 62:191-217; Ivics, Z. (1997) Cell 91:501-510; Boulay, J-L. and Récipon, H. (1998) Curr. Opin. Biotechnol. 9:445-450).

Expression vectors that may be effective for the expression of mddt include, but are not limited to, the PCDNA 3.1, EPITAG, PRCCMV2, PREP, PVAX vectors (Invitrogen, Carlsbad CA), PCMV-SCRIPT, PCMV-TAG, PEGSH/PERV (Stratagene, La Jolla CA), and PTET-OFF,

PTET-ON, PTRE2, PTRE2-LUC, PTK-HYG (Clontech, Palo Alto CA). The mddt of the invention may be expressed using (i) a constitutively active promoter, (e.g., from cytomegalovirus (CMV), Rous sarcoma virus (RSV), SV40 virus, thymidine kinase (TK), or β-actin genes), (ii) an inducible promoter (e.g., the tetracycline-regulated promoter (Gossen, M. and Bujard, H. (1992) Proc. Natl. Acad. Sci. U.S.A. 89:5547-5551; Gossen, M. et al., (1995) Science 268:1766-1769; Rossi, F.M.V. and Blau, H.M. (1998) Curr. Opin. Biotechnol. 9:451-456), commercially available in the T-REX plasmid (Invitrogen); the ecdysone-inducible promoter (available in the plasmids PVGRXR and PIND; Invitrogen); the FK506/rapamycin inducible promoter; or the RU486/mifepristone inducible promoter (Rossi, F.M.V. and Blau, H.M. supra), or (iii) a tissue-specific promoter or the native promoter of the endogenous gene encoding MDDT from a normal individual.

Commercially available liposome transformation kits (e.g., the PERFECT LIPID TRANSFECTION KIT, available from Invitrogen) allow one with ordinary skill in the art to deliver polynucleotides to target cells in culture and require minimal effort to optimize experimental parameters. In the alternative, transformation is performed using the calcium phosphate method (Graham, F.L. and Eb, A.J. (1973) Virology 52:456-467), or by electroporation (Neumann, E. et al. (1982) EMBO J. 1:841-845). The introduction of DNA to primary cells requires modification of these standardized mammalian transfection protocols.

In another embodiment of the invention, diseases or disorders caused by genetic defects with respect to mddt expression are treated by constructing a retrovirus vector consisting of (i) mddt under the control of an independent promoter or the retrovirus long terminal repeat (LTR) promoter, (ii) appropriate RNA packaging signals, and (iii) a Rev-responsive element (RRE) along with additional retrovirus *cis*-acting RNA sequences and coding sequences required for efficient vector propagation. Retrovirus vectors (e.g., PFB and PFBNEO) are commercially available (Stratagene) and are based on published data (Riviere, I. et al. (1995) Proc. Natl. Acad. Sci. U.S.A. 92:6733-6737), incorporated by reference herein. The vector is propagated in an appropriate vector producing cell line (VPCL) that expresses an envelope gene with a tropism for receptors on the target cells or a promiscuous envelope protein such as VSVg (Armentano, D. et al. (1987) J. Virol. 61:1647-1650; Bender, M.A. et al. (1987) J. Virol. 61:1639-1646; Adam, M.A. and Miller, A.D. (1988) J. Virol. 62:3802-3806; Dull, T. et al. (1998) J. Virol. 72:8463-8471; Zufferey, R. et al. (1998) J. Virol. 72:9873-9880). U.S. Patent Number 5,910,434 to Rigg ("Method for obtaining retrovirus packaging cell lines producing high transducing efficiency retroviral supernatant") discloses a method for obtaining retrovirus packaging cell lines and is hereby incorporated by reference. Propagation of retrovirus vectors, transduction of a population of cells (e.g., $CD4^+$ T-cells), and the return of transduced cells to a patient are procedures well known to persons skilled in the art of gene therapy and have been well documented (Ranga, U. et al. (1997) J. Virol. 71:7020-7029; Bauer, G. et al. (1997) Blood 89:2259-2267;

Bonyhadi, M.L. (1997) J. Virol. 71:4707-4716; Ranga, U. et al. (1998) Proc. Natl. Acad. Sci. U.S.A. 95:1201-1206; Su, L. (1997) Blood 89:2283-2290).

In the alternative, an adenovirus-based gene therapy delivery system is used to deliver mddt to cells which have one or more genetic abnormalities with respect to the expression of mddt. The construction and packaging of adenovirus-based vectors are well known to those with ordinary skill in the art. Replication defective adenovirus vectors have proven to be versatile for importing genes encoding immunoregulatory proteins into intact islets in the pancreas (Csete, M.E. et al. (1995) Transplantation 27:263-268). Potentially useful adenoviral vectors are described in U.S. Patent Number 5,707,618 to Armentano ("Adenovirus vectors for gene therapy"), hereby incorporated by reference. For adenoviral vectors, see also Antinozzi, P.A. et al. (1999) Annu. Rev. Nutr. 19:511-544 and Verma, I.M. and Somia, N. (1997) Nature 18:389:239-242, both incorporated by reference herein.

In another alternative, a herpes-based, gene therapy delivery system is used to deliver mddt to target cells which have one or more genetic abnormalities with respect to the expression of mddt. The use of herpes simplex virus (HSV)-based vectors may be especially valuable for introducing mddt to cells of the central nervous system, for which HSV has a tropism. The construction and packaging of herpes-based vectors are well known to those with ordinary skill in the art. A replication-competent herpes simplex virus (HSV) type 1-based vector has been used to deliver a reporter gene to the eyes of primates (Liu, X. et al. (1999) Exp. Eye Res.169:385-395). The construction of a HSV-1 virus vector has also been disclosed in detail in U.S. Patent Number 5,804,413 to DeLuca ("Herpes simplex virus strains for gene transfer"), which is hereby incorporated by reference. U.S. Patent Number 5,804,413 teaches the use of recombinant HSV d92 which consists of a genome containing at least one exogenous gene to be transferred to a cell under the control of the appropriate promoter for purposes including human gene therapy. Also taught by this patent are the construction and use of recombinant HSV strains deleted for ICP4, ICP27 and ICP22. For HSV vectors, see also Goins, W. F. et al. 1999 J. Virol. 73:519-532 and Xu, H. et al., (1994) Dev. Biol. 163:152-161, hereby incorporated by reference. The manipulation of cloned herpesvirus sequences, the generation of recombinant virus following the transfection of multiple plasmids containing different segments of the large herpesvirus genomes, the growth and propagation of herpesvirus, and the infection of cells with herpesvirus are techniques well known to those of ordinary skill in the art.

In another alternative, an alphavirus (positive, single-stranded RNA virus) vector is used to deliver mddt to target cells. The biology of the prototypic alphavirus, Semliki Forest Virus (SFV), has been studied extensively and gene transfer vectors have been based on the SFV genome (Garoff, H. and Li, K-J. (1998) Curr. Opin. Biotech. 9:464-469). During alphavirus RNA replication, a subgenomic RNA is generated that normally encodes the viral capsid proteins. This subgenomic RNA replicates to higher levels than the full-length genomic RNA, resulting in the overproduction of

capsid proteins relative to the viral proteins with enzymatic activity (e.g., protease and polymerase). Similarly, inserting mddt into the alphavirus genome in place of the capsid-coding region results in the production of a large number of mddt RNAs and the synthesis of high levels of MDDT in vector transduced cells. While alphavirus infection is typically associated with cell lysis within a few days, the ability to establish a persistent infection in hamster normal kidney cells (BHK-21) with a variant of Sindbis virus (SIN) indicates that the lytic replication of alphaviruses can be altered to suit the needs of the gene therapy application (Dryga, S.A. et al. (1997) Virology 228:74-83). The wide host range of alphaviruses will allow the introduction of mddt into a variety of cell types. The specific transduction of a subset of cells in a population may require the sorting of cells prior to transduction. The methods of manipulating infectious cDNA clones of alphaviruses, performing alphavirus cDNA and RNA transfections, and performing alphavirus infections, are well known to those with ordinary skill in the art.

Antibodies

Anti-MDDT antibodies may be used to analyze protein expression levels. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, and Fab fragments. For descriptions of and protocols of antibody technologies, see, e.g., Pound J.D. (1998) Immunochemical Protocols, Humana Press, Totowa, NJ.

The amino acid sequence encoded by the mddt of the Sequence Listing may be analyzed by appropriate software (e.g., LASERGENE NAVIGATOR software, DNASTAR) to determine regions of high immunogenicity. The optimal sequences for immunization are selected from the C-terminus, the N-terminus, and those intervening, hydrophilic regions of the polypeptide which are likely to be exposed to the external environment when the polypeptide is in its natural conformation. Analysis used to select appropriate epitopes is also described by Ausubel (1997, supra, Chapter 11.7). Peptides used for antibody induction do not need to have biological activity; however, they must be antigenic. Peptides used to induce specific antibodies may have an amino acid sequence consisting of at least five amino acids, preferably at least 10 amino acids, and most preferably at least 15 amino acids. A peptide which mimics an antigenic fragment of the natural polypeptide may be fused with another protein such as keyhole hemolimpet cyanin (KLH; Sigma, St. Louis MO) for antibody production. A peptide encompassing an antigenic region may be expressed from an mddt, synthesized as described above, or purified from human cells.

Procedures well known in the art may be used for the production of antibodies. Various hosts including mice, goats, and rabbits, may be immunized by injection with a peptide. Depending on the host species, various adjuvants may be used to increase immunological response.

In one procedure, peptides about 15 residues in length may be synthesized using an ABI 431A peptide synthesizer (Applied Biosystems) using fmoc-chemistry and coupled to KLH (Sigma) by reaction with M-maleimidobenzoyl-N-hydroxysuccinimide ester (Ausubel, 1995, supra). Rabbits are immunized with the peptide-KLH complex in complete Freund's adjuvant. The resulting antisera are tested for antipeptide activity by binding the peptide to plastic, blocking with 1% bovine serum albumin (BSA), reacting with rabbit antisera, washing, and reacting with radioiodinated goat anti-rabbit IgG. Antisera with antipeptide activity are tested for anti-MDDT activity using protocols well known in the art, including ELISA, radioimmunoassay (RIA), and immunoblotting.

In another procedure, isolated and purified peptide may be used to immunize mice (about 100 μg of peptide) or rabbits (about 1 mg of peptide). Subsequently, the peptide is radioiodinated and used to screen the immunized animals' B-lymphocytes for production of antipeptide antibodies. Positive cells are then used to produce hybridomas using standard techniques. About 20 mg of peptide is sufficient for labeling and screening several thousand clones. Hybridomas of interest are detected by screening with radioiodinated peptide to identify those fusions producing peptide-specific monoclonal antibody. In a typical protocol, wells of a multi-well plate (FAST, Becton-Dickinson, Palo Alto, CA) are coated with affinity-purified, specific rabbit-anti-mouse (or suitable anti-species IgG) antibodies at 10 mg/ml. The coated wells are blocked with 1% BSA and washed and exposed to supernatants from hybridomas. After incubation, the wells are exposed to radiolabeled peptide at 1 mg/ml.

Clones producing antibodies bind a quantity of labeled peptide that is detectable above background. Such clones are expanded and subjected to 2 cycles of cloning. Cloned hybridomas are injected into pristane-treated mice to produce ascites, and monoclonal antibody is purified from the ascitic fluid by affinity chromatography on protein A (Amersham Pharmacia Biotech). Several procedures for the production of monoclonal antibodies, including in vitro production, are described in Pound (supra). Monoclonal antibodies with antipeptide activity are tested for anti-MDDT activity using protocols well known in the art, including ELISA, RIA, and immunoblotting.

Antibody fragments containing specific binding sites for an epitope may also be generated. For example, such fragments include, but are not limited to, the F(ab')2 fragments produced by pepsin digestion of the antibody molecule, and the Fab fragments generated by reducing the disulfide bridges of the F(ab')2 fragments. Alternatively, construction of Fab expression libraries in filamentous bacteriophage allows rapid and easy identification of monoclonal fragments with desired specificity (Pound, supra, Chaps. 45-47). Antibodies generated against polypeptide encoded by mddt can be used to purify and characterize full-length MDDT protein and its activity, binding partners, etc.

Assays Using Antibodies

Anti-MDDT antibodies may be used in assays to quantify the amount of MDDT found in a particular human cell. Such assays include methods utilizing the antibody and a label to detect expression level under normal or disease conditions. The peptides and antibodies of the invention may be used with or without modification or labeled by joining them, either covalently or noncovalently, with a reporter molecule.

Protocols for detecting and measuring protein expression using either polyclonal or monoclonal antibodies are well known in the art. Examples include ELISA, RIA, and fluorescent activated cell sorting (FACS). Such immunoassays typically involve the formation of complexes between the MDDT and its specific antibody and the measurement of such complexes. These and other assays are described in Pound (supra).

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

The disclosures of all patents, applications and publications, mentioned above and below, including U.S. Ser. No. 60/349,946 and U.S. 60/349,413, are hereby expressly incorporated by reference.

EXAMPLES

I. Construction of cDNA Libraries

RNA was purchased from CLONTECH Laboratories, Inc. (Palo Alto CA) or isolated from various tissues. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIZOL (Life Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA purity. In most cases, RNA was treated with DNase. For most libraries, poly(A+) RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega Corporation (Promega), Madison WI), OLIGOTEX latex particles (QIAGEN, Inc. (QIAGEN), Valencia CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA purification kit (Ambion, Inc., Austin TX).

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP vector system (Stratagene Cloning Systems, Inc. (Stratagene), La Jolla CA) or SUPERSCRIPT

plasmid system (Life Technologies), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, supra, Chapters 5.1 through 6.6.) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., PBLUESCRIPT plasmid (Stratagene), PSPORT1 plasmid (Life Technologies), PCDNA2.1 plasmid (Invitrogen, Carlsbad CA), PBK-CMV plasmid (Stratagene), PCR2-TOPOTA plasmid (Invitrogen), PCMV-ICIS plasmid (Stratagene), pIGEN (Incyte Genomics, Palo Alto CA), pRARE (Incyte Genomics), or pINCY (Incyte Genomics), or derivatives thereof. Recombinant plasmids were transformed into competent E. coli cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5α, DH10B, or ElectroMAX DH10B from Life Technologies.

II. Isolation of cDNA Clones

Plasmids were recovered from host cells by in vivo excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using at least one of the following: the Magic or WIZARD Minipreps DNA purification system (Promega); the AGTC Miniprep purification kit (Edge BioSystems, Gaithersburg MD); and the QIAWELL 8, QIAWELL 8 Plus, and QIAWELL 8 Ultra plasmid purification systems or the R.E.A.L. PREP 96 plasmid purification kit (QIAGEN). Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format. (Rao, V.B. (1994) Anal. Biochem. 216:1-14.) Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Inc. (Molecular Probes), Eugene OR) and a FLUOROSKAN II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

III. Sequencing and Analysis

cDNA sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 thermal cycler (Applied Biosystems) or the PTC-200 thermal cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific Corp., Sunnyvale CA) or the MICROLAB 2200 liquid transfer system (Hamilton). cDNA

sequencing reactions were prepared using reagents provided by Amersham Pharmacia Biotech or supplied in ABI sequencing kits such as the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems). Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system (Molecular Dynamics); the ABI PRISM 373 or 377 sequencing system (Applied Biosystems) in conjunction with standard ABI protocols and base calling software; or other sequence analysis systems known in the art. Reading frames within the cDNA sequences were identified using standard methods (reviewed in Ausubel, 1997, supra, Chapter 7.7). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example VIII.

IV. Assembly and Analysis of Sequences

Component sequences from chromatograms were subject to PHRED analysis and assigned a quality score. The sequences having at least a required quality score were subject to various pre-processing editing pathways to eliminate, e.g., low quality 3' ends, vector and linker sequences, polyA tails, Alu repeats, mitochondrial and ribosomal sequences, bacterial contamination sequences, and sequences smaller than 50 base pairs. In particular, low-information sequences and repetitive elements (e.g., dinucleotide repeats, Alu repeats, etc.) were replaced by "n's", or masked, to prevent spurious matches.

Processed sequences were then subject to assembly procedures in which the sequences were assigned to gene bins (bins). Each sequence could only belong to one bin. Sequences in each gene bin were assembled to produce consensus sequences (templates). Subsequent new sequences were added to existing bins using BLASTN (v.1.4 WashU) and CROSSMATCH. Candidate pairs were identified as all BLAST hits having a quality score greater than or equal to 150. Alignments of at least 82% local identity were accepted into the bin. The component sequences from each bin were assembled using a version of PHRAP. Bins with several overlapping component sequences were assembled using DEEP PHRAP. The orientation (sense or antisense) of each assembled template was determined based on the number and orientation of its component sequences. Template sequences as disclosed in the sequence listing correspond to sense strand sequences (the "forward" reading frames), to the best determination. The complementary (antisense) strands are inherently disclosed herein. The component sequences which were used to assemble each template consensus sequence are listed in Table 5, along with their positions along the template nucleotide sequences.

Bins were compared against each other and those having local similarity of at least 82% were combined and reassembled. Reassembled bins having templates of insufficient overlap (less than 95% local identity) were re-split. Assembled templates were also subject to analysis by STITCHER/EXON MAPPER algorithms which analyze the probabilities of the presence of splice

variants, alternatively spliced exons, splice junctions, differential expression of alternative spliced genes across tissue types or disease states, etc. These resulting bins were subject to several rounds of the above assembly procedures.

Once gene bins were generated based upon sequence alignments, bins were clone joined based upon clone information. If the 5' sequence of one clone was present in one bin and the 3' sequence from the same clone was present in a different bin, it was likely that the two bins actually belonged together in a single bin. The resulting combined bins underwent assembly procedures to regenerate the consensus sequences.

The final assembled templates were subsequently annotated using the following procedure. Template sequences were analyzed using BLASTN (v2.0, NCBI) versus gbpri (GenBank version 135). "Hits" were defined as an exact match having from 95% local identity over 200 base pairs through 100% local identity over 100 base pairs, or a homolog match having an E-value, i.e. a probability score, of $\leq 1 \times 10^{-8}$. The hits were subject to frameshift FASTx versus GENPEPT (GenBank version 135). (See Table 8). In this analysis, a homolog match was defined as having an E-value of $\leq 1 \times 10^{-8}$. The assembly method used above was described in "System and Methods for Analyzing Biomolecular Sequences," U.S.S.N. 09/276,534, filed March 25, 1999, and the LIFESEQ Gold user manual (Incyte) both incorporated by reference herein.

Following assembly, template sequences were subjected to motif, BLAST, and functional analyses, and categorized in protein hierarchies using methods described in, e.g., "Database System Employing Protein Function Hierarchies for Viewing Biomolecular Sequence Data," U.S. Patent Number 6,023,659; "Relational Database for Storing Biomolecule Information," U.S.S.N. 08/947,845, filed October 9, 1997; "Project-Based Full-Length Biomolecular Sequence Database," U.S. Patent Number 5,953,727; and "Relational Database and System for Storing Information Relating to Biomolecular Sequences," U.S.S.N. 09/034,807, filed March 4, 1998, all of which are incorporated by reference herein.

The template sequences were further analyzed by translating each template in all three forward reading frames and searching each translation against the Pfam database of hidden Markov model-based protein families and domains using the HMMER software package (available to the public from Washington University School of Medicine, St. Louis MO). Regions of templates which, when translated, contain similarity to Pfam consensus sequences are reported in Table 3, along with descriptions of Pfam protein domains and families. Only those Pfam hits with an E-value of $\leq 1 \times 10^{-3}$ are reported. (See also World Wide Web site http://pfam.wustl.edu/ for detailed descriptions of Pfam protein domains and families.)

Additionally, the template sequences were translated in all three forward reading frames, and each translation was searched against hidden Markov models for signal peptides using the HMMER

software package. Construction of hidden Markov models and their usage in sequence analysis has been described. (See, for example, Eddy, S.R. (1996) Curr. Opin. Str. Biol. 6:361-365.) Only those signal peptide hits with a cutoff score of 11 bits or greater are reported. A cutoff score of 11 bits or greater corresponds to at least about 91-94% true-positives in signal peptide prediction. Template sequences were also translated in all three forward reading frames, and each translation was searched against TMHMMER, a program that uses a hidden Markov model (HMM) to delineate transmembrane segments on protein sequences and determine orientation (Sonnhammer, E.L. et al. (1998) Proc. Sixth Intl. Conf. On Intelligent Systems for Mol. Biol., Glasgow et al., eds., The Am. Assoc. for Artificial Intelligence (AAAI) Press, Menlo Park, CA, and MIT Press, Cambridge, MA, pp. 175-182.) Regions of templates which, when translated, contain similarity to signal peptide or transmembrane consensus sequences are reported in Table 4.

The results of HMMER analysis as reported in Tables 3 and 4 may support the results of BLAST analysis as reported in Table 2 or may suggest alternative or additional properties of template-encoded polypeptides not previously uncovered by BLAST or other analyses.

Template sequences are further analyzed using the bioinformatics tools listed in Table 8, or using sequence analysis software known in the art such as MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Template sequences may be further queried against public databases such as the GenBank rodent, mammalian, vertebrate, prokaryote, and eukaryote databases.

The template sequences were translated to derive the corresponding longest open reading frame as presented by the polypeptide sequences as reported in Table 7. Alternatively, a polypeptide of the invention may begin at any of the methionine residues within the full length translated polypeptide. Polypeptide sequences were subsequently analyzed by querying against the GenBank protein database (GENPEPT, (GenBank version 135)). Full length polynucleotide sequences are also analyzed using MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Polynucleotide and polypeptide sequence alignments are generated using default parameters specified by the CLUSTAL algorithm as incorporated into the MEGALIGN multisequence alignment program (DNASTAR), which also calculates the percent identity between aligned sequences.

Table 7 shows sequences with homology to the polypeptides of the invention as identified by BLAST analysis against the GenBank protein (GENPEPT) database. Column 1 shows the polypeptide sequence identification number (SEQ ID NO:) for the polypeptide segments of the invention. Column 2 shows the reading frame used in the translation of the polynucleotide sequences encoding the polypeptide segments. Column 3 shows the length of the translated polypeptide segments. Columns 4 and 5 show the start and stop nucleotide positions of the polynucleotide

sequences encoding the polypeptide segments. Column 6 shows the GenBank identification number (GI Number) of the nearest GenBank homolog. Column 7 shows the probability score for the match between each polypeptide and its GenBank homolog. Column 8 shows the annotation of the GenBank homolog.

V. Analysis of Polynucleotide Expression

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound. (See, e.g., Sambrook, supra, ch. 7; Ausubel, 1995, supra, ch. 4 and 16.)

Analogous computer techniques applying BLAST were used to search for identical or related molecules in cDNA databases such as GenBank or LIFESEQ (Incyte Genomics). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

$$\frac{\text{BLAST Score x Percent Identity}}{\text{5 x minimum \{length(Seq. 1), length(Seq. 2)\}}}$$

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. The product score is a normalized value between 0 and 100, and is calculated as follows: the BLAST score is multiplied by the percent nucleotide identity and the product is divided by (5 times the length of the shorter of the two sequences). The BLAST score is calculated by assigning a score of +5 for every base that matches in a high-scoring segment pair (HSP), and -4 for every mismatch. Two sequences may share more than one HSP (separated by gaps). If there is more than one HSP, then the pair with the highest BLAST score is used to calculate the product score. The product score represents a balance between fractional overlap and quality in a BLAST alignment. For example, a product score of 100 is produced only for 100% identity over the entire length of the shorter of the two sequences being compared. A product score of 70 is produced either by 100% identity and 70% overlap at one end, or by 88% identity and 100% overlap at the other. A product score of 50 is produced either by 100% identity and 50% overlap at one end, or 79% identity and 100% overlap.

VI. Tissue Distribution Profiling

A tissue distribution profile is determined for each template by compiling the cDNA library tissue classifications of its component cDNA sequences. Each component sequence, is derived from

a cDNA library constructed from a human tissue. Each human tissue is classified into one of the following categories: cardiovascular system; connective tissue; digestive system; embryonic structures; endocrine system; exocrine glands; genitalia, female; genitalia, male; germ cells; hemic and immune system; liver; musculoskeletal system; nervous system; pancreas; respiratory system; sense organs; skin; stomatognathic system; unclassified/mixed; or urinary tract. Template sequences, component sequences, and cDNA library/tissue information are found in the LIFESEQ GOLD database (Incyte Genomics, Palo Alto CA).

Table 6 shows the tissue distribution profile for the templates of the invention. For each template, the three most frequently observed tissue categories are shown in column 3, along with the percentage of component sequences belonging to each category. Only tissue categories with percentage values of ≥10% are shown. A tissue distribution of "widely distributed" in column 3 indicates percentage values of <10% in all tissue categories.

VII. Transcript Image Analysis

Transcript images are generated as described in Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent Number 5,840,484, incorporated herein by reference.

VIII. Extension of Polynucleotide Sequences and Isolation of a Full-length cDNA

Oligonucleotide primers designed using an mddt of the Sequence Listing are used to extend the nucleic acid sequence. One primer is synthesized to initiate 5' extension of the template, and the other primer, to initiate 3' extension of the template. The initial primers may be designed using OLIGO 4.06 software (National Biosciences, Inc. (National Biosciences), Plymouth MN), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations are avoided. Selected human cDNA libraries are used to extend the sequence. If more than one extension is necessary or desired, additional or nested sets of primers are designed.

High fidelity amplification is obtained by PCR using methods well known in the art. PCR is performed in 96-well plates using the PTC-200 thermal cycler (MJ Research). The reaction mix contains DNA template, 200 nmol of each primer, reaction buffer containing Mg^{2+}, $(NH_4)_2SO_4$, and ß-mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme (Life Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ are as follows: Step 1: 94°C, 3 min; Step 2:

94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well is determined by dispensing 100 μl PICOGREEN quantitation reagent (0.25% (v/v); Molecular Probes) dissolved in 1X Tris-EDTA (TE) and 0.5 μl of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Incorporated (Corning), Corning NY), allowing the DNA to bind to the reagent. The plate is scanned in a FLUOROSKAN II (Labsystems Oy) to measure the fluorescence of the sample and to quantify the concentration of DNA. A 5 μl to 10 μl aliquot of the reaction mixture is analyzed by electrophoresis on a 1 % agarose mini-gel to determine which reactions are successful in extending the sequence.

The extended nucleotides are desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For shotgun sequencing, the digested nucleotides are separated on low concentration (0.6 to 0.8%) agarose gels, fragments are excised, and agar digested with AGAR ACE (Promega). Extended clones are religated using T4 ligase (New England Biolabs, Inc., Beverly MA) into pUC 18 vector (Amersham Pharmacia Biotech), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction site overhangs, and transfected into competent E. coli cells. Transformed cells are selected on antibiotic-containing media, individual colonies are picked and cultured overnight at 37°C in 384-well plates in LB/2x carbenicillin liquid media.

The cells are lysed, and DNA is amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA is quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries are reamplified using the same conditions as described above. Samples are diluted with 20% dimethysulfoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems).

In like manner, the mddt is used to obtain regulatory sequences (promoters, introns, and enhancers) using the procedure above, oligonucleotides designed for such extension, and an appropriate genomic library.

IX. Labeling of Probes and Southern Hybridization Analyses

Hybridization probes derived from the mddt of the Sequence Listing are employed for screening cDNAs, mRNAs, or genomic DNA. The labeling of probe nucleotides between 100 and

1000 nucleotides in length is specifically described, but essentially the same procedure may be used with larger cDNA fragments. Probe sequences are labeled at room temperature for 30 minutes using a T4 polynucleotide kinase, γ^{32}P-ATP, and 0.5X One-Phor-All Plus (Amersham Pharmacia Biotech) buffer and purified using a ProbeQuant G-50 Microcolumn (Amersham Pharmacia Biotech). The probe mixture is diluted to 10^7 dpm/μg/ml hybridization buffer and used in a typical membrane-based hybridization analysis.

The DNA is digested with a restriction endonuclease such as Eco RV and is electrophoresed through a 0.7% agarose gel. The DNA fragments are transferred from the agarose to nylon membrane (NYTRAN Plus, Schleicher & Schuell, Inc., Keene NH) using procedures specified by the manufacturer of the membrane. Prehybridization is carried out for three or more hours at 68°C, and hybridization is carried out overnight at 68°C. To remove non-specific signals, blots are sequentially washed at room temperature under increasingly stringent conditions, up to 0.1x saline sodium citrate (SSC) and 0.5% sodium dodecyl sulfate. After the blots are placed in a PHOSPHORIMAGER cassette (Molecular Dynamics) or are exposed to autoradiography film, hybridization patterns of standard and experimental lanes are compared. Essentially the same procedure is employed when screening RNA.

X. Chromosome Mapping of mddt

The cDNA sequences which were used to assemble SEQ ID NO:1-104 are compared with sequences from the Incyte LIFESEQ database and public domain databases using BLAST and other implementations of the Smith-Waterman algorithm. Sequences from these databases that match SEQ ID NO:1-104 are assembled into clusters of contiguous and overlapping sequences using assembly algorithms such as PHRAP (Table 8). Radiation hybrid and genetic mapping data available from public resources such as the Stanford Human Genome Center (SHGC), Whitehead Institute for Genome Research (WIGR), and Généthon are used to determine if any of the clustered sequences have been previously mapped. Inclusion of a mapped sequence in a cluster will result in the assignment of all sequences of that cluster, including its particular SEQ ID NO:, to that map location. The genetic map locations of SEQ ID NO:1-104 are described as ranges, or intervals, of human chromosomes. The map position of an interval, in centiMorgans, is measured relative to the terminus of the chromosome's p-arm. (The centiMorgan (cM) is a unit of measurement based on recombination frequencies between chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase (Mb) of DNA in humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Généthon which provide boundaries for radiation hybrid markers whose sequences were included in each of the clusters.

XI. Microarray Analysis

Probe Preparation from Tissue or Cell Samples

Total RNA is isolated from tissue samples using the guanidinium thiocyanate method and polyA$^+$ RNA is purified using the oligo (dT) cellulose method. Each polyA$^+$ RNA sample is reverse transcribed using MMLV reverse-transcriptase, 0.05 pg/μl oligo-dT primer (21mer), 1X first strand buffer, 0.03 units/μl RNase inhibitor, 500 μM dATP, 500 μM dGTP, 500 μM dTTP, 40 μM dCTP, 40 μM dCTP-Cy3 (BDS) or dCTP-Cy5 (Amersham Pharmacia Biotech). The reverse transcription reaction is performed in a 25 ml volume containing 200 ng polyA$^+$ RNA with GEMBRIGHT kits (Incyte). Specific control polyA$^+$ RNAs are synthesized by in vitro transcription from non-coding yeast genomic DNA (W. Lei, unpublished). As quantitative controls, the control mRNAs at 0.002 ng, 0.02 ng, 0.2 ng, and 2 ng are diluted into reverse transcription reaction at ratios of 1:100,000, 1:10,000, 1:1000, 1:100 (w/w) to sample mRNA respectively. The control mRNAs are diluted into reverse transcription reaction at ratios of 1:3, 3:1, 1:10, 10:1, 1:25, 25:1 (w/w) to sample mRNA differential expression patterns. After incubation at 37° C for 2 hr, each reaction sample (one with Cy3 and another with Cy5 labeling) is treated with 2.5 ml of 0.5M sodium hydroxide and incubated for 20 minutes at 85° C to the stop the reaction and degrade the RNA. Probes are purified using two successive CHROMA SPIN 30 gel filtration spin columns (CLONTECH Laboratories, Inc. (CLONTECH), Palo Alto CA) and after combining, both reaction samples are ethanol precipitated using 1 ml of glycogen (1 mg/ml), 60 ml sodium acetate, and 300 ml of 100% ethanol. The probe is then dried to completion using a SpeedVAC (Savant Instruments Inc., Holbrook NY) and resuspended in 14 μl 5X SSC/0.2% SDS.

Microarray Preparation

Sequences of the present invention are used to generate array elements. Each array element is amplified from bacterial cells containing vectors with cloned cDNA inserts. PCR amplification uses primers complementary to the vector sequences flanking the cDNA insert. Array elements are amplified in thirty cycles of PCR from an initial quantity of 1-2 ng to a final quantity greater than 5 μg. Amplified array elements are then purified using SEPHACRYL-400 (Amersham Pharmacia Biotech).

Purified array elements are immobilized on polymer-coated glass slides. Glass microscope slides (Corning) are cleaned by ultrasound in 0.1% SDS and acetone, with extensive distilled water washes between and after treatments. Glass slides are etched in 4% hydrofluoric acid (VWR Scientific Products Corporation (VWR), West Chester, PA), washed extensively in distilled water, and coated with 0.05% aminopropyl silane (Sigma) in 95% ethanol. Coated slides are cured in a 110°C oven.

Array elements are applied to the coated glass substrate using a procedure described in US Patent No. 5,807,522, incorporated herein by reference. 1 μl of the array element DNA, at an average concentration of 100 ng/μl, is loaded into the open capillary printing element by a high-speed robotic apparatus. The apparatus then deposits about 5 nl of array element sample per slide.

Microarrays are UV-crosslinked using a STRATALINKER UV-crosslinker (Stratagene). Microarrays are washed at room temperature once in 0.2% SDS and three times in distilled water. Non-specific binding sites are blocked by incubation of microarrays in 0.2% casein in phosphate buffered saline (PBS) (Tropix, Inc., Bedford, MA) for 30 minutes at 60° C followed by washes in 0.2% SDS and distilled water as before.

Hybridization

Hybridization reactions contain 9 μl of probe mixture consisting of 0.2 μg each of Cy3 and Cy5 labeled cDNA synthesis products in 5X SSC, 0.2% SDS hybridization buffer. The probe mixture is heated to 65° C for 5 minutes and is aliquoted onto the microarray surface and covered with an 1.8 cm^2 coverslip. The arrays are transferred to a waterproof chamber having a cavity just slightly larger than a microscope slide. The chamber is kept at 100% humidity internally by the addition of 140 μl of 5x SSC in a corner of the chamber. The chamber containing the arrays is incubated for about 6.5 hours at 60° C. The arrays are washed for 10 min at 45° C in a first wash buffer (1X SSC, 0.1% SDS), three times for 10 minutes each at 45° C in a second wash buffer (0.1X SSC), and dried.

Detection

Reporter-labeled hybridization complexes are detected with a microscope equipped with an Innova 70 mixed gas 10 W laser (Coherent, Inc., Santa Clara CA) capable of generating spectral lines at 488 nm for excitation of Cy3 and at 632 nm for excitation of Cy5. The excitation laser light is focused on the array using a 20X microscope objective (Nikon, Inc., Melville NY). The slide containing the array is placed on a computer-controlled X-Y stage on the microscope and raster-scanned past the objective. The 1.8 cm x 1.8 cm array used in the present example is scanned with a resolution of 20 micrometers.

In two separate scans, a mixed gas multiline laser excites the two fluorophores sequentially. Emitted light is split, based on wavelength, into two photomultiplier tube detectors (PMT R1477, Hamamatsu Photonics Systems, Bridgewater NJ) corresponding to the two fluorophores. Appropriate filters positioned between the array and the photomultiplier tubes are used to filter the signals. The emission maxima of the fluorophores used are 565 nm for Cy3 and 650 nm for Cy5. Each array is typically scanned twice, one scan per fluorophore using the appropriate filters at the laser source, although the apparatus is capable of recording the spectra from both fluorophores simultaneously.

The sensitivity of the scans is typically calibrated using the signal intensity generated by a cDNA control species added to the probe mix at a known concentration. A specific location on the array contains a complementary DNA sequence, allowing the intensity of the signal at that location to be correlated with a weight ratio of hybridizing species of 1:100,000. When two probes from different sources (e.g., representing test and control cells), each labeled with a different fluorophore, are hybridized to a single array for the purpose of identifying genes that are differentially expressed, the calibration is done by labeling samples of the calibrating cDNA with the two fluorophores and adding identical amounts of each to the hybridization mixture.

The output of the photomultiplier tube is digitized using a 12-bit RTI-835H analog-to-digital (A/D) conversion board (Analog Devices, Inc., Norwood, MA) installed in an IBM-compatible PC computer. The digitized data are displayed as an image where the signal intensity is mapped using a linear 20-color transformation to a pseudocolor scale ranging from blue (low signal) to red (high signal). The data is also analyzed quantitatively. Where two different fluorophores are excited and measured simultaneously, the data are first corrected for optical crosstalk (due to overlapping emission spectra) between the fluorophores using each fluorophore's emission spectrum.

A grid is superimposed over the fluorescence signal image such that the signal from each spot is centered in each element of the grid. The fluorescence signal within each element is then integrated to obtain a numerical value corresponding to the average intensity of the signal. The software used for signal analysis is the GEMTOOLS gene expression analysis program (Incyte Genomics). Array elements that exhibit at least about a two-fold change in expression, a signal-to-background ratio of at least about 2.5, and an element spot size of at least about 40%, are considered to be differentially expressed.).

XII. Complementary Nucleic Acids

Sequences complementary to the mddt are used to detect, decrease, or inhibit expression of the naturally occurring nucleotide. The use of oligonucleotides comprising from about 15 to 30 base pairs is typical in the art. However, smaller or larger sequence fragments can also be used. Appropriate oligonucleotides are designed from the mddt using OLIGO 4.06 software (National Biosciences) or other appropriate programs and are synthesized using methods standard in the art or ordered from a commercial supplier. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent transcription factor binding to the promoter sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding and processing of the transcript.

XIII. Expression of MDDT

Expression and purification of MDDT is accomplished using bacterial or virus-based expression systems. For expression of MDDT in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac* (*tac*) hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria express MDDT upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of MDDT in eukaryotic cells is achieved by infecting insect or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding MDDT by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See e.g., Engelhard, supra; and Sandig, supra.)

In most expression systems, MDDT is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step, affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from MDDT at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak Company, Rochester NY). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, supra, Chapters 10 and 16). Purified MDDT obtained by these methods can be used directly in the following activity assay.

XIV. Demonstration of MDDT Activity

MDDT, or biologically active fragments thereof, are labeled with ^{125}I Bolton-Hunter reagent. (See, e.g., Bolton, A.E. and W.M. Hunter (1973) Biochem. J. 133:529-539.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled MDDT, washed, and any wells with labeled MDDT complex are assayed. Data obtained using different

concentrations of MDDT are used to calculate values for the number, affinity, and association of MDDT with the candidate molecules.

Alternatively, molecules interacting with MDDT are analyzed using the yeast two-hybrid system as described in Fields, S. and O. Song (1989) Nature 340:245-246, or using commercially available kits based on the two-hybrid system, such as the MATCHMAKER system (CLONTECH).

MDDT may also be used in the PATHCALLING process (CuraGen Corp., New Haven CT) which employs the yeast two-hybrid system in a high-throughput manner to determine all interactions between the proteins encoded by two large libraries of genes (Nandabalan, K. et al. (2000) U.S. Patent No. 6,057,101).

XV. Functional Assays

MDDT function is assessed by expressing mddt at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include pCMV SPORT (Life Technologies) and pCR3.1 (Invitrogen Corporation, Carlsbad CA), both of which contain the cytomegalovirus promoter. 5-10 μg of recombinant vector are transiently transfected into a human cell line, preferably of endothelial or hematopoietic origin, using either liposome formulations or electroporation. 1-2 μg of an additional plasmid containing sequences encoding a marker protein are co-transfected.

Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; CLONTECH), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties.

FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M. G. (1994) Flow Cytometry, Oxford, New York NY.

The influence of MDDT on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding MDDT and either CD64 or CD64-GFP.

CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Inc., Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding MDDT and other genes of interest can be analyzed by northern analysis or microarray techniques.

XVI. Production of Antibodies

MDDT substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) Methods Enzymol. 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

Alternatively, the MDDT amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding peptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel, 1995, supra, Chapter 11.)

Typically, peptides 15 residues in length are synthesized using an ABI 431A peptide synthesizer (Applied Biosystems) using fmoc-chemistry and coupled to KLH (Sigma) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, supra.) Rabbits are immunized with the peptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for antipeptide activity by, for example, binding the peptide to plastic, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG. Antisera with antipeptide activity are tested for anti-MDDT activity using protocols well known in the art, including ELISA, RIA, and immunoblotting.

XVII. Purification of Naturally Occurring MDDT Using Specific Antibodies

Naturally occurring or recombinant MDDT is substantially purified by immunoaffinity chromatography using antibodies specific for MDDT. An immunoaffinity column is constructed by covalently coupling anti-MDDT antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing MDDT are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of MDDT (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt

antibody/MDDT binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and MDDT is collected.

All publications and patents mentioned in the above specification are herein incorporated by reference. Various modifications and variations of the described method and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the above-described modes for carrying out the invention which are obvious to those skilled in the field of molecular biology or related fields are intended to be within the scope of the following claims.

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
1	LG:1447398.9:2002JAN18	105	LG:1447398.9.orf2:2002JAN18
2	LG:201488.3:2002JAN18	106	LG:201488.3.orf3:2002JAN18
3	LG:288410.6:2002JAN18	107	LG:288410.6.orf2:2002JAN18
4	LG:7682817.1:2002JAN18	108	LG:7682817.1.orf3:2002JAN18
5	LG:7685059.6:2002JAN18	109	LG:7685059.6.orf2:2002JAN18
6	LG:7689671.1:2002JAN18	110	LG:7689671.1.orf2:2002JAN18
7	LG:7689684.1:2002JAN18	111	LG:7689684.1.orf2:2002JAN18
8	LG:7762669.1:2002JAN18	112	LG:7762669.1.orf1:2002JAN18
9	LG:965822.1:2002JAN18	113	LG:965822.1.orf1:2002JAN18
10	LG:006394.31:2002JAN18	114	LG:006394.31.orf2:2002JAN18
11	LG:018258.1:2002JAN18	115	LG:018258.1.orf2:2002JAN18
12	LG:027320.5:2002JAN18	116	LG:027320.5.orf3:2002JAN18
13	LG:057499.1:2002JAN18	117	LG:057499.1.orf1:2002JAN18
14	LG:065935.21:2002JAN18	118	LG:065935.21.orf2:2002JAN18
15	LG:071860.12:2002JAN18	119	LG:071860.12.orf3:2002JAN18
16	LG:087383.29:2002JAN18	120	LG:087383.29.orf2:2002JAN18
17	LG:098580.3:2002JAN18	121	LG:098580.3.orf2:2002JAN18
18	LG:1001879.1:2002JAN18	122	LG:1001879.1.orf1:2002JAN18
19	LG:1079456.4:2002JAN18	123	LG:1079456.4.orf3:2002JAN18
20	LG:1080598.9:2002JAN18	124	LG:1080598.9.orf2:2002JAN18
21	LG:1090358.10:2002JAN18	125	LG:1090358.10.orf1:2002JAN18
22	LG:1097492.2:2002JAN18	126	LG:1097492.2.orf2:2002JAN18
23	LG:1099945.26:2002JAN18	127	LG:1099945.26.orf2:2002JAN18
24	LG:110016.1:2002JAN18	128	LG:110016.1.orf1:2002JAN18
25	LG:1137613.10:2002JAN18	129	LG:1137613.10.orf2:2002JAN18
26	LG:118836.26:2002JAN18	130	LG:118836.26.orf2:2002JAN18
27	LG:1330261.32:2002JAN18	131	LG:1330261.32.orf1:2002JAN18
28	LG:1347461.28:2002JAN18	132	LG:1347461.28.orf3:2002JAN18
29	LG:1383494.16:2002JAN18	133	LG:1383494.16.orf3:2002JAN18
30	LG:1400155.1:2002JAN18	134	LG:1400155.1.orf2:2002JAN18
31	LG:1446621.1:2002JAN18	135	LG:1446621.1.orf3:2002JAN18
32	LG:144920.1:2002JAN18	136	LG:144920.1.orf1:2002JAN18
33	LG:1452619.1:2002JAN18	137	LG:1452619.1.orf2:2002JAN18
34	LG:1453417.6:2002JAN18	138	LG:1453417.6.orf1:2002JAN18
35	LG:148485.8:2002JAN18	139	LG:148485.8.orf1:2002JAN18
36	LG:1502670.1:2002JAN18	140	LG:1502670.1.orf2:2002JAN18
37	LG:206593.3:2002JAN18	141	LG:206593.3.orf2:2002JAN18
38	LG:228273.22:2002JAN18	142	LG:228273.22.orf1:2002JAN18
39	LG:228319.2:2002JAN18	143	LG:228319.2.orf1:2002JAN18
40	LG:229165.16:2002JAN18	144	LG:229165.16.orf2:2002JAN18
41	LG:230895.9:2002JAN18	145	LG:230895.9.orf1:2002JAN18
42	LG:233552.5:2002JAN18	146	LG:233552.5.orf1:2002JAN18
43	LG:234430.7:2002JAN18	147	LG:234430.7.orf3:2002JAN18
44	LG:236659.1:2002JAN18	148	LG:236659.1.orf3:2002JAN18
45	LG:236767.26:2002JAN18	149	LG:236767.26.orf2:2002JAN18
46	LG:237489.7:2002JAN18	150	LG:237489.7.orf1:2002JAN18
47	LG:238218.20:2002JAN18	151	LG:238218.20.orf1:2002JAN18
48	LG:239939.14:2002JAN18	152	LG:239939.14.orf3:2002JAN18
49	LG:242288.11:2002JAN18	153	LG:242288.11.orf1:2002JAN18
50	LG:242491.29:2002JAN18	154	LG:242491.29.orf1:2002JAN18

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
51	LG:243488.41:2002JAN18	155	LG:243488.41.orf3:2002JAN18
52	LG:247792.18:2002JAN18	156	LG:247792.18.orf2:2002JAN18
53	LG:253193.17:2002JAN18	157	LG:253193.17.orf3:2002JAN18
54	LG:257088.20:2002JAN18	158	LG:257088.20.orf2:2002JAN18
55	LG:265552.1:2002JAN18	159	LG:265552.1.orf2:2002JAN18
56	LG:275355.12:2002JAN18	160	LG:275355.12.orf1:2002JAN18
57	LG:280014.1:2002JAN18	161	LG:280014.1.orf1:2002JAN18
58	LG:299937.3:2002JAN18	162	LG:299937.3.orf3:2002JAN18
59	LG:311197.3:2002JAN18	163	LG:311197.3.orf3:2002JAN18
60	LG:321069.2:2002JAN18	164	LG:321069.2.orf1:2002JAN18
61	LG:330900.8:2002JAN18	165	LG:330900.8.orf2:2002JAN18
62	LG:330931.9:2002JAN18	166	LG:330931.9.orf1:2002JAN18
63	LG:330985.1:2002JAN18	167	LG:330985.1.orf3:2002JAN18
64	LG:332027.9:2002JAN18	168	LG:332027.9.orf3:2002JAN18
65	LG:335377.8:2002JAN18	169	LG:335377.8.orf2:2002JAN18
66	LG:337452.25:2002JAN18	170	LG:337452.25.orf3:2002JAN18
67	LG:340580.16:2002JAN18	171	LG:340580.16.orf2:2002JAN18
68	LG:350272.6:2002JAN18	172	LG:350272.6.orf2:2002JAN18
69	LG:397228.1:2002JAN18	173	LG:397228.1.orf1:2002JAN18
70	LG:401325.41:2002JAN18	174	LG:401325.41.orf2:2002JAN18
71	LG:402029.14:2002JAN18	175	LG:402029.14.orf3:2002JAN18
72	LG:407233.2:2002JAN18	176	LG:407233.2.orf3:2002JAN18
73	LG:407346.1:2002JAN18	177	LG:407346.1.orf3:2002JAN18
74	LG:407689.7:2002JAN18	178	LG:407689.7.orf3:2002JAN18
75	LG:407700.1:2002JAN18	179	LG:407700.1.orf2:2002JAN18
76	LG:410461.92:2002JAN18	180	LG:410461.92.orf3:2002JAN18
77	LG:411043.3:2002JAN18	181	LG:411043.3.orf2:2002JAN18
78	LG:438690.47:2002JAN18	182	LG:438690.47.orf1:2002JAN18
79	LG:444677.81:2002JAN18	183	LG:444677.81.orf1:2002JAN18
80	LG:457464.24:2002JAN18	184	LG:457464.24.orf3:2002JAN18
81	LG:7684793.15:2002JAN18	185	LG:7684793.15.orf3:2002JAN18
82	LG:7687485.1:2002JAN18	186	LG:7687485.1.orf1:2002JAN18
83	LG:7689661.4:2002JAN18	187	LG:7689661.4.orf2:2002JAN18
84	LG:7690373.1:2002JAN18	188	LG:7690373.1.orf1:2002JAN18
85	LG:7696560.1:2002JAN18	189	LG:7696560.1.orf3:2002JAN18
86	LG:7698190.26:2002JAN18	190	LG:7698190.26.orf3:2002JAN18
87	LG:7763560.12:2002JAN18	191	LG:7763560.12.orf1:2002JAN18
88	LG:7763587.20:2002JAN18	192	LG:7763587.20.orf2:2002JAN18
89	LG:899263.10:2002JAN18	193	LG:899263.10.orf2:2002JAN18
90	LG:977837.31:2002JAN18	194	LG:977837.31.orf1:2002JAN18
91	LG:978560.13:2002JAN18	195	LG:978560.13.orf2:2002JAN18
92	LG:979390.2:2002JAN18	196	LG:979390.2.orf1:2002JAN18
93	LG:983019.1:2002JAN18	197	LG:983019.1.orf2:2002JAN18
94	LG:997202.7:2002JAN18	198	LG:997202.7.orf2:2002JAN18
95	LG:998756.3:2002JAN18	199	LG:998756.3.orf1:2002JAN18
96	LG:103460.28:2002JAN18	200	LG:103460.28.orf2:2002JAN18
97	LG:1501505.19:2002JAN18	201	LG:1501505.19.orf1:2002JAN18
98	LG:233444.9:2002JAN18	202	LG:233444.9.orf2:2002JAN18
99	LG:234824.7:2002JAN18	203	LG:234824.7.orf2:2002JAN18
100	LG:235708.23:2002JAN18	204	LG:235708.23.orf1:2002JAN18

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
101	LG:236649.14:2002JAN18	205	LG:236649.14.orf1:2002JAN18
102	LG:332474.7:2002JAN18	206	LG:332474.7.orf1:2002JAN18
103	LG:335727.8:2002JAN18	207	LG:335727.8.orf2:2002JAN18
104	LG:481983.1:2002JAN18	208	LG:481983.1.orf3:2002JAN18

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
1	LG:1447398.9:2002JAN18	g21748992	0.00	Homo sapiens cDNA FLJ33450 fis, clone BRAMY2000025.
2	LG:201488.3:2002JAN18	g6599307	4.00E-98	LIM domains containing protein 1 (Mus musculus)
3	LG:288410.6:2002JAN18	g15823642	0.00	ALS2CR7 (Homo sapiens)
4	LG:7682817.1:2002JAN18	g18203798	1.00E-97	Homo sapiens, clone MGC:15956 IMAGE:3538227, mRNA, complete cds.
5	LG:7685059.6:2002JAN18	g21750806	0.00	Homo sapiens cDNA FLJ34942 fis, clone NT2RP7007530, moderately similar to ZINC FINGER PROTEIN 211.
6	LG:7689671.1:2002JAN18	g22477160	8.00E-45	Homo sapiens, clone IMAGE:4846514, mRNA, partial cds.
7	LG:7689684.1:2002JAN18	g21750781	0.00	Homo sapiens cDNA FLJ34921 fis, clone NT2RP7002978, moderately similar to ZINC FINGER PROTEIN ZFP-36.
8	LG:7762669.1:2002JAN18	g21754721	1.00E-85	Homo sapiens cDNA FLJ38144 fis, clone D9OST2003397, moderately similar to ZINC FINGER PROTEIN 91.
9	LG:965822.1:2002JAN18	g21955442	0.00	Homo sapiens, Similar to zinc finger protein 331; zinc finger protein 463, clone IMAGE:3920900, mRNA.
10	LG:006394.31:2002JAN18	g20987337	0.00	Homo sapiens, clone IMAGE:4748060, mRNA, partial cds.
11	LG:018258.1:2002JAN18	g19483967	1.00E-110	RIKEN cDNA 0610009A07 gene (Mus musculus)
12	LG:027320.5:2002JAN18	g9967126	0.00	Macaca fascicularis brain cDNA, clone:QccE-17586.
13	LG:057499.1:2002JAN18	g12407440	0.00	Homo sapiens tripartite motif protein TRIM33 alpha (TRIM33) mRNA, complete cds; alternatively spliced.
14	LG:065935.21:2002JAN18	g23273088	0.00	Homo sapiens, clone MGC:43081 IMAGE:5259721, mRNA, complete cds.
15	LG:071860.12:2002JAN18	g17390472	1.00E-123	Homo sapiens, mago-nashi (Drosophila) homolog, proliferation-associated, clone MGC:17367 IMAGE:3861094, mRNA, complete cds.
16	LG:087383.29:2002JAN18	g12053194	0.00	Homo sapiens mRNA; cDNA DKFZp434H1130 (from clone DKFZp434H1130); complete cds.
17	LG:098580.3:2002JAN18	g20069117	0.00	Homo sapiens caspase 12 variant alpha (CASP12) mRNA, complete sequence; alternatively spliced.
18	LG:1001879.1:2002JAN18	g21886479	0.00	unnamed protein product (Homo sapiens)
19	LG:1079456.4:2002JAN18	g22760915	0.00	Homo sapiens cDNA FLJ90585 fis, clone PLACE1000907, highly similar to ZINC FINGER PROTEIN 83.
20	LG:1080598.9:2002JAN18	g21618498	0.00	Homo sapiens, Similar to hypothetical protein FLJ20079, clone MGC:45408 IMAGE:5540009, mRNA, complete cds.

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
21	LG:1090358.10:2002JAN18	g21749606	0.00	Homo sapiens cDNA FLJ33955 fis, clone CTONG2018652, moderately similar to ZINC FINGER PROTEIN MFG-3.
22	LG:1097492.2:2002JAN18	g10047329	0.00	KIAA1626 protein (Homo sapiens)
23	LG:1099945.26:2002JAN18	g6808024	0.00	Homo sapiens mRNA; cDNA DKFZp434J0428 (from clone DKFZp434J0428).
24	LG:110016.1:2002JAN18	g16552018	0.00	Homo sapiens cDNA FLJ32015 fis, clone NTONG1000052, weakly similar to Rattus norvegicus mRNA for Kelch related protein 1.
25	LG:1137613.10:2002JAN18	g14789616	1.00E-175	Homo sapiens, Similar to RIKEN cDNA 6720463E02 gene, clone MGC:17810 IMAGE:3891655, mRNA, complete cds.
26	LG:118836.26:2002JAN18	g12667437	0.00	Homo sapiens NIR3 mRNA, complete cds.
27	LG:1330261.32:2002JAN18	g22761032	0.00	unnamed protein product (Homo sapiens)
28	LG:1347461.28:2002JAN18	g21755436	0.00	Homo sapiens cDNA FLJ38725 fis, clone KIDNE2010265.
29	LG:1383494.16:2002JAN18	g16741479	0.00	Homo sapiens, CGI-100 protein, clone MGC:5366 IMAGE:3048959, mRNA, complete cds.
30	LG:1400155.1:2002JAN18	g556220	0.00	Human NAD+-dependent succinate-semialdehyde dehydrogenase (SSADH) mRNA, 3' end.
31	LG:1446621.1:2002JAN18	g16306805	1.00E-105	Homo sapiens, zinc finger protein 43 (HTF6), clone MGC:10581 IMAGE:3687640, mRNA, complete cds.
32	LG:144920.1:2002JAN18	g2689444	1.00E-141	ZNF134 (Homo sapiens)
33	LG:1452619.1:2002JAN18	g9246972	0.00	Homo sapiens RNA-binding protein BRUNOL2 (BRUNOL2) mRNA, complete cds.
34	LG:1453417.6:2002JAN18	g1665821	0.00	Similar to D.melanogaster cadherin-related tumor suppressor (Homo sapiens)
35	LG:148485.8:2002JAN18	g21595467	0.00	Homo sapiens, clone MGC:40579 IMAGE:5217372, mRNA, complete cds.
36	LG:1502670.1:2002JAN18	g21755190	0.00	Homo sapiens cDNA FLJ38528 fis, clone HCHON2000942.
37	LG:206593.3:2002JAN18	g16551839	0.00	Homo sapiens cDNA FLJ31875 fis, clone NT2RP7002450, weakly similar to ZINC FINGER PROTEIN 84.
38	LG:228273.22:2002JAN18	g3327175	0.00	Homo sapiens mRNA for KIAA0681 protein, partial cds.
39	LG:228319.2:2002JAN18	g21752073	0.00	unnamed protein product (Homo sapiens)
40	LG:229165.16:2002JAN18	g3970716	0.00	Homo sapiens mRNA for KET protein.
41	LG:230895.9:2002JAN18	g15620894	0.00	Homo sapiens mRNA for KIAA1918 protein, partial cds.
42	LG:233552.5:2002JAN18	g10047282	0.00	Homo sapiens mRNA for KIAA1604 protein, partial cds.

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
43	LG:234430.7:2002JAN18	g12653106	0.00	Homo sapiens, hypothetical protein dJ37E16.5, clone MGC:8472 IMAGE:2821743, mRNA, complete cds.
44	LG:236659.1:2002JAN18	g12083895	0.00	Homo sapiens polybromo-1 (PB1) mRNA, complete cds, alternatively spliced.
45	LG:236767.26:2002JAN18	g18916868	0.00	Homo sapiens mRNA for KIAA1978 protein.
46	LG:237489.7:2002JAN18	g16588680	0.00	Homo sapiens anion transporter/exchanger-9 (SLC26A9) mRNA, complete
47	LG:238218.20:2002JAN18	g19116222	0.00	Homo sapiens, clone MGC:9833 IMAGE:3863491, mRNA, complete cds.
48	LG:239939.14:2002JAN18	g21758739	0.00	Homo sapiens cDNA FLJ25797 fis, clone TST07046.
49	LG:242288.11:2002JAN18	g4164385	0.00	PAK4 protein (Homo sapiens)
50	LG:242491.29:2002JAN18	g22760074	0.00	Homo sapiens cDNA FLJ90076 fis, clone HEMBA1004444, moderately similar to GLYCOPROTEIN 25L PRECURSOR.
51	LG:243488.41:2002JAN18	g21542540	0.00	Homo sapiens, Similar to HTPAP protein, clone MGC:32924 IMAGE:5267610, mRNA, complete cds.
52	LG:247792.18:2002JAN18	g21739660	0.00	Homo sapiens mRNA; cDNA DKFZp434L1426 (from clone DKFZp434L1426).
53	LG:253193.17:2002JAN18	g20988139	0.00	Homo sapiens, E74-like factor 1 (ets domain transcription factor), clone MGC:40398 IMAGE:4385989, mRNA, complete cds.
54	LG:257088.20:2002JAN18	g20372683	0.00	euchromatic histone methyltransferase 1 (Homo sapiens)
55	LG:265552.1:2002JAN18	g18490501	1.00E-100	RIKEN cDNA 2010002A20 gene (Mus musculus)
56	LG:275355.12:2002JAN18	g17223623	0.00	Homo sapiens ATP-binding cassette A9 mRNA, complete cds.
57	LG:280014.1:2002JAN18	g18088579	0.00	Homo sapiens, clone MGC:23949 IMAGE:4243903, mRNA, complete cds.
58	LG:299937.3:2002JAN18	g10439753	0.00	Homo sapiens cDNA: FLJ23158 fis, clone LNG09623.
59	LG:311197.3:2002JAN18	g21750727	0.00	Homo sapiens cDNA FLJ34876 fis, clone NT2NE2015362, moderately similar to Mitogen inducible gene mig-2.
60	LG:321069.2:2002JAN18	g18677068	0.00	Homo sapiens cDNA FLJ23877 fis, clone LNG13624.
61	LG:330900.8:2002JAN18	g18043698	0.00	PRO2000 protein (Homo sapiens)
62	LG:330931.9:2002JAN18	g16551908	0.00	Homo sapiens cDNA FLJ31930 fis, clone NT2RP7006162, weakly similar to ZINC FINGER PROTEIN MFG-3.
63	LG:330985.1:2002JAN18	g1222522	0.00	Human placental folate transporter (hFOLT1) mRNA, complete cds.
64	LG:332027.9:2002JAN18	g21749635	0.00	Homo sapiens cDNA FLJ33979 fis, clone DFNES2004371.
65	LG:335377.8:2002JAN18	g16550148	0.00	Homo sapiens cDNA FLJ30864 fis, clone FEBRA2004091, highly similar to Homo sapiens RING finger protein terf mRNA.

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
66	LG:337452.25:2002JAN18	g16549250	0.00	Homo sapiens cDNA FLJ30100 fis, clone BNGH41000104.
67	LG:340580.16:2002JAN18	g10434656	0.00	Homo sapiens cDNA FLJ12900 fis, clone NT2RP2004321.
68	LG:350272.6:2002JAN18	g22859174	0.00	hypothetical protein (Homo sapiens)
69	LG:397228.1:2002JAN18	g15741221	1.00E-17	gene overexpressed in astrocytoma (Homo sapiens)
70	LG:401325.41:2002JAN18	g4126475	0.00	BAP2-alpha protein (Homo sapiens)
71	LG:402029.14:2002JAN18	g10437932	0.00	Homo sapiens cDNA: FLJ21771 fis, clone COLF7779.
72	LG:407233.2:2002JAN18	g20810035	0.00	Homo sapiens, Fc receptor-like protein 3, clone MGC:34866 IMAGE:4340939, mRNA, complete cds.
73	LG:407346.1:2002JAN18	g21753085	0.00	unnamed protein product (Homo sapiens)
74	LG:407689.7:2002JAN18	g13365844	0.00	Macaca fascicularis brain cDNA clone:QccE-19502, full insert sequence.
75	LG:407700.1:2002JAN18	g14198271	0.00	Homo sapiens, clone MGC:5352 IMAGE:3048106, mRNA, complete cds.
76	LG:410461.92:2002JAN18	g16877725	0.00	Homo sapiens, likely ortholog of mouse g1-related zinc finger protein, clone MGC:15167 IMAGE:3535930, mRNA, complete cds.
77	LG:411043.3:2002JAN18	g21755898	0.00	unnamed protein product (Homo sapiens)
78	LG:438690.47:2002JAN18	g10434222	0.00	Homo sapiens cDNA FLJ12622 fis, clone NT2RM4001731, highly similar to Homo sapiens F-box protein Lilina (LILINA) mRNA.
79	LG:444677.81:2002JAN18	g4929678	0.00	Homo sapiens CGI-105 protein mRNA, complete cds.
80	LG:457464.24:2002JAN18	g12653266	0.00	Homo sapiens, fusion, derived from t(12;16) malignant liposarcoma, clone MGC:8537 IMAGE:2822692, mRNA, complete cds.
81	LG:7684793.15:2002JAN18	g12275895	0.00	tripartite motif protein TRIM19 gamma (Homo sapiens)
82	LG:7687485.1:2002JAN18	g21752508	0.00	Homo sapiens cDNA FLJ36280 fis, clone THYMU2003282, moderately similar to ZINC FINGER PROTEIN 135.
83	LG:7689661.4:2002JAN18	g21739829	0.00	Homo sapiens mRNA; cDNA DKFZp761C148 (from clone DKFZp761C148); complete cds.
84	LG:7690373.1:2002JAN18	g21757678	0.00	Homo sapiens cDNA FLJ40479 fis, clone TESTI2043282, moderately similar to ZINC FINGER PROTEIN 43.
85	LG:7696560.1:2002JAN18	g21752388	0.00	Homo sapiens cDNA FLJ36178 fis, clone TESTI2026534.
86	LG:7698190.26:2002JAN18	g4914583	0.00	Homo sapiens mRNA; cDNA DKFZp586A032 (from clone DKFZp586A032); partial cds.
87	LG:7763560.12:2002JAN18	g12005677	0.00	Homo sapiens HT029 mRNA, complete cds.

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
88	LG:7763587.20:2002JAN18	g12803700	0.00	Homo sapiens, ankyrin repeat-containing protein, clone MGC:3528 IMAGE:3607648, mRNA, complete cds.
89	LG:899263.10:2002JAN18	g21750988	0.00	Homo sapiens cDNA FLJ35084 fis, clone PLACE6005482.
90	LG:977837.31:2002JAN18	g22760683	0.00	Homo sapiens cDNA FLJ90440 fis, clone NT2RP3000921, weakly similar to TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.
91	LG:978560.13:2002JAN18	g10047251	0.00	KIAA1588 protein (Homo sapiens)
92	LG:979390.2:2002JAN18	g21756044	1.00E-180	Homo sapiens cDNA FLJ39208 fis, clone OCBBF2006030.
93	LG:983019.1:2002JAN18	g23336960	0.00	Homo sapiens, Similar to eomesodermin homolog (Xenopus laevis), clone IMAGE:5223017, mRNA.
94	LG:997202.7:2002JAN18	g12803934	0.00	Homo sapiens, clone IMAGE:3638276, mRNA, partial cds.
95	LG:998756.3:2002JAN18	g24181969	0.00	NEW1 domain containing protein isoform (Homo sapiens)
96	LG:103460.28:2002JAN18	g7023281	0.00	Homo sapiens cDNA FLJ10927 fis, clone OVARC1000466.
97	LG:1501505.19:2002JAN18	g15929456	0.00	Homo sapiens, clone IMAGE:3885940, mRNA, partial cds.
98	LG:233444.9:2002JAN18	g7023136	0.00	unnamed protein product (Homo sapiens)
99	LG:234824.7:2002JAN18	g15879022	0.00	Homo sapiens genomic sequence surrounding NotI site, clone NL1-CP10R.
100	LG:235708.23:2002JAN18	g22760880	0.00	Homo sapiens cDNA FLJ90562 fis, clone OVARC1001163.
101	LG:236649.14:2002JAN18	g20067239	1.00E-118	putative regulation protein GS3 (Rattus norvegicus)
102	LG:332474.7:2002JAN18	g21755742	0.00	Homo sapiens cDNA FLJ38969 fis, clone NT2RI2002359.
103	LG:335727.8:2002JAN18	g16554117	0.00	Homo sapiens cDNA FLJ25361 fis, clone TST01713.
104	LG:481983.1:2002JAN18	g21410797	0.00	Homo sapiens, clone IMAGE:4396549, mRNA, partial cds.

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
1	LG:1447398.9:2002JAN18	677	754	forward 2	RPEL	RPEL repeat	7.40E-14
2	LG:201488.3:2002JAN18	57	233	forward 3	LIM	LIM domain	2.10E-29
3	LG:288410.6:2002JAN18	443	1099	forward 2	pkinase	Protein kinase domain	7.40E-05
3	LG:288410.6:2002JAN18	243	1091	forward 3	pkinase	Protein kinase domain	3.70E-09
4	LG:7682817.1:2002JAN18	898	1074	forward 1	Ribosomal_S5	Ribosomal protein S5, N-terminal domain	0.00051
5	LG:7685059.6:2002JAN18	314	436	forward 2	KRAB	KRAB box	1.90E-24
6	LG:7689671.1:2002JAN18	317	439	forward 2	KRAB	KRAB box	1.90E-26
7	LG:7689684.1:2002JAN18	188	310	forward 2	KRAB	KRAB box	8.20E-24
8	LG:7762669.1:2002JAN18	178	300	forward 1	KRAB	KRAB box	2.90E-26
9	LG:965822.1:2002JAN18	424	546	forward 1	KRAB	KRAB box	6.50E-25
10	LG:006394.31:2002JAN18	1790	2248	forward 2	RhoGAP	RhoGAP domain	6.10E-57
10	LG:006394.31:2002JAN18	228	317	forward 3	WW	WW domain	3.20E-05
11	LG:018258.1:2002JAN18	299	718	forward 2	Nitroreductase	Nitroreductase family	9.50E-05
12	LG:027320.5:2002JAN18	132	332	forward 3	SAM	SAM domain (Sterile alpha motif)	6.30E-06
13	LG:057499.1:2002JAN18	1306	1575	forward 1	bromodomain	Bromodomain	4.10E-18
13	LG:057499.1:2002JAN18	1087	1224	forward 1	PHD	PHD-finger	2.70E-12
14	LG:065935.21:2002JAN18	209	517	forward 2	HesB-like	HesB-like domain	3.50E-36
15	LG:071860.12:2002JAN18	426	773	forward 3	Mago_nashi	Mago nashi protein	2.40E-19
16	LG:087383.29:2002JAN18	173	439	forward 2	FCH	Fes/CIP4 homology domain	2.90E-30
17	LG:098580.3:2002JAN18	74	331	forward 2	ICE_p10	ICE-like protease (caspase) p10 domain	1.30E-31
18	LG:1001879.1:2002JAN18	310	381	forward 1	LRR	Leucine Rich Repeat	1.60E-40
18	LG:1001879.1:2002JAN18	217	306	forward 1	LRRNT	Leucine rich repeat N-terminal domain	4.40E-07
18	LG:1001879.1:2002JAN18	1204	1365	forward 1	LRRCT	Leucine rich repeat C-terminal domain	7.20E-05
19	LG:1079456.4:2002JAN18	398	520	forward 2	KRAB	KRAB box	1.00E-28
19	LG:1079456.4:2002JAN18	183	305	forward 3	KRAB	KRAB box	4.00E-24
20	LG:1080598.9:2002JAN18	755	823	forward 2	zf-C2H2	Zinc finger, C2H2 type	8.00E-59
20	LG:1080598.9:2002JAN18	524	646	forward 2	KRAB	KRAB box	1.80E-22
21	LG:1090358.10:2002JAN18	808	930	forward 1	KRAB	KRAB box	3.90E-27
21	LG:1090358.10:2002JAN18	1285	1353	forward 1	zf-C2H2	Zinc finger, C2H2 type	1.20E-22
21	LG:1090358.10:2002JAN18	1452	1520	forward 3	zf-C2H2	Zinc finger, C2H2 type	5.80E-52
22	LG:1097492.2:2002JAN18	691	1194	forward 1	RhoGEF	RhoGEF domain	2.00E-05

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
23	LG:1099945.26:2002JAN18	236	364	forward 2	Ribosomal_L37e	Ribosomal protein L37e	1.80E-06
24	LG:110016.1:2002JAN18	1337	1477	forward 2	Kelch	Kelch motif	1.30E-23
24	LG:110016.1:2002JAN18	135	452	forward 3	BTB	BTB/POZ domain	8.40E-35
25	LG:1137613.10:2002JAN18	152	415	forward 2	Dynein_light	Dynein light chain type 1	7.40E-20
26	LG:118836.26:2002JAN18	1084	1770	forward 1	DDHD	DDHD domain	1.10E-42
27	LG:1330261.32:2002JAN18	5538	5615	forward 3	calponin	Calponin family repeat	4.20E-11
27	LG:1330261.32:2002JAN18	5109	5441	forward 3	CH	Calponin homology (CH) domain	1.30E-06
28	LG:1347461.28:2002JAN18	864	1385	forward 3	DUF152	Uncharacterized ACR, YfiH family COG1496	6.90E-07
29	LG:1383494.16:2002JAN18	219	890	forward 3	EMP24_GP25L	emp24/gp25L/p24 family	9.90E-15
30	LG:1400155.1:2002JAN18	164	1408	forward 2	aldedh	Aldehyde dehydrogenase family	1.90E-115
31	LG:1446621.1:2002JAN18	777	899	forward 3	KRAB	KRAB box	4.00E-23
32	LG:144920.1:2002JAN18	184	252	forward 1	zf-C2H2	Zinc finger, C2H2 type	3.60E-71
33	LG:1452619.1:2002JAN18	179	403	forward 2	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	2.90E-50
34	LG:1453417.6:2002JAN18	2374	2643	forward 1	cadherin	Cadherin domain	1.10E-76
34	LG:1453417.6:2002JAN18	7342	8073	forward 1	7tm_2	7 transmembrane receptor (Secretin family)	4.00E-57
34	LG:1453417.6:2002JAN18	3919	4080	forward 1	EGF	EGF-like domain	4.30E-31
34	LG:1453417.6:2002JAN18	7168	7329	forward 1	GPS	Latrophilin/CL-1-like GPS domain	1.50E-27
34	LG:1453417.6:2002JAN18	4408	4896	forward 1	laminin_G	Laminin G domain	4.60E-18
34	LG:1453417.6:2002JAN18	6142	6315	forward 1	HRM	Hormone receptor domain	1.60E-17
34	LG:1453417.6:2002JAN18	1436	1714	forward 2	cadherin	Cadherin domain	2.20E-81
34	LG:1453417.6:2002JAN18	780	1064	forward 3	cadherin	Cadherin domain	8.10E-27
35	LG:148485.8:2002JAN18	64	852	forward 1	FGGY	FGGY family of carbohydrate kinases, N-terminal domain	2.70E-45
35	LG:148485.8:2002JAN18	859	1551	forward 1	FGGY_C	FGGY family of carbohydrate kinases, C-terminal domain	1.10E-25
36	LG:1502670.1:2002JAN18	2	568	forward 2	arf	ADP-ribosylation factor family	1.10E-10
37	LG:206593.3:2002JAN18	307	375	forward 1	zf-C2H2	Zinc finger, C2H2 type	1.60E-11
37	LG:206593.3:2002JAN18	476	544	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.00E-46
37	LG:206593.3:2002JAN18	54	122	forward 3	zf-C2H2	Zinc finger, C2H2 type	2.00E-21
38	LG:228273.22:2002JAN18	877	1098	forward 1	mbt	mbt repeat	1.00E-138

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
38	LG:228273.22:2002JAN18	1801	1896	forward 1	zf-C2HC	Zinc finger, C2HC type	3.40E-11
38	LG:228273.22:2002JAN18	2194	2388	forward 1	SAM	SAM domain (Sterile alpha motif)	7.70E-08
39	LG:228319.2:2002JAN18	835	1056	forward 1	mbt	mbt repeat	9.50E-81
39	LG:228319.2:2002JAN18	1470	1679	forward 3	mbt	mbt repeat	1.60E-38
40	LG:229165.16:2002JAN18	155	1465	forward 2	P53	P53	4.00E-196
41	LG:230895.9:2002JAN18	73	627	forward 1	Glycos_transf_2	Glycosyl transferase	5.60E-37
41	LG:230895.9:2002JAN18	1012	1137	forward 1	Ricin_B_lectin	QXW lectin repeat	7.70E-35
42	LG:233552.5:2002JAN18	874	1425	forward 1	MIF4G	MIF4G domain	4.80E-37
42	LG:233552.5:2002JAN18	1750	2070	forward 1	MA3	MA3 domain	1.90E-25
43	LG:234430.7:2002JAN18	123	848	forward 3	Hydrolase	haloacid dehalogenase-like hydrolase	1.80E-21
44	LG:236659.1:2002JAN18	300	569	forward 3	bromodomain	Bromodomain	6.50E-182
44	LG:236659.1:2002JAN18	3018	3374	forward 3	BAH	BAH domain	6.60E-87
44	LG:236659.1:2002JAN18	4290	4463	forward 3	HMG_box	HMG (high mobility group) box	0.00015
45	LG:236767.26:2002JAN18	197	391	forward 2	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	1.10E-26
46	LG:237489.7:2002JAN18	424	951	forward 1	STAS	STAS domain	2.00E-20
47	LG:238218.20:2002JAN18	250	372	forward 1	KRAB	KRAB box	3.70E-14
47	LG:238218.20:2002JAN18	1225	1779	forward 1	CENP-B	CENP-B protein	0.00056
48	LG:239939.14:2002JAN18	378	875	forward 3	ras	Ras family	1.90E-30
49	LG:242288.11:2002JAN18	700	1455	forward 1	pkinase	Protein kinase domain	1.10E-62
50	LG:242491.29:2002JAN18	70	663	forward 1	EMP24_GP25L	emp24/gp25L/p24 family	3.00E-33
51	LG:243488.41:2002JAN18	198	644	forward 3	PAP2	PAP2 superfamily	1.60E-32
52	LG:247792.18:2002JAN18	569	1711	forward 2	RNB	RNB-like protein	2.40E-115
53	LG:253193.17:2002JAN18	1854	2111	forward 3	Ets	Ets-domain	1.00E-51
54	LG:257088.20:2002JAN18	3230	3328	forward 2	ank	Ankyrin repeat	7.50E-32
54	LG:257088.20:2002JAN18	3531	3629	forward 3	ank	Ankyrin repeat	2.30E-09
55	LG:265552.1:2002JAN18	242	427	forward 2	ig	Immunoglobulin domain	7.00E-10
56	LG:275355.12:2002JAN18	49	468	forward 1	ABC_tran	ABC transporter	1.50E-06
57	LG:280014.1:2002JAN18	481	1005	forward 1	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	1.10E-16
58	LG:299937.3:2002JAN18	405	518	forward 3	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	2.50E-06
58	LG:299937.3:2002JAN18	1008	1118	forward 3	zf-B_box	B-box zinc finger	0.00055

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
59	LG:311197.3:2002JAN18	1497	1808	forward 3	PH	PH domain	1.40E-09
60	LG:321069.2:2002JAN18	544	837	forward 1	mito_carr	Mitochondrial carrier protein	7.70E-30
61	LG:330900.8:2002JAN18	965	1537	forward 2	AAA	ATPase family associated with various cellular activities (AAA)	1.10E-80
61	LG:330900.8:2002JAN18	2546	2821	forward 2	bromodomain	Bromodomain	7.60E-15
62	LG:330931.9:2002JAN18	1	60	forward 1	zf-C2H2	Zinc finger, C2H2 type	2.60E-39
63	LG:330985.1:2002JAN18	186	1421	forward 3	Folate_carrier	Reduced folate carrier	5.00E-292
64	LG:332027.9:2002JAN18	303	1286	forward 3	Methyltransf_5	MraW methylase family	1.00E-90
65	LG:335377.8:2002JAN18	476	601	forward 2	zf-B_box	B-box zinc finger	2.50E-15
65	LG:335377.8:2002JAN18	242	391	forward 2	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.60E-12
65	LG:335377.8:2002JAN18	1671	2033	forward 3	SPRY	SPRY domain	5.60E-18
66	LG:337452.25:2002JAN18	3	590	forward 3	pkinase	Protein kinase domain	2.80E-10
67	LG:340580.16:2002JAN18	1049	1639	forward 2	PBX	PBX domain	6.10E-31
67	LG:340580.16:2002JAN18	1643	1822	forward 2	homeobox	Homeobox domain	1.20E-17
68	LG:350272.6:2002JAN18	947	1315	forward 2	SPRY	SPRY domain	1.10E-10
69	LG:397228.1:2002JAN18	49	165	forward 1	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.10E-11
70	LG:401325.41:2002JAN18	1260	1436	forward 3	SH3	SH3 domain	0.00011
71	LG:402029.14:2002JAN18	879	1304	forward 3	Cation_ATPase_C	Cation transporting ATPase, C-terminus	4.00E-40
72	LG:407233.2:2002JAN18	366	542	forward 3	ig	Immunoglobulin domain	1.80E-20
73	LG:407346.1:2002JAN18	285	602	forward 3	CH	Calponin homology (CH) domain	5.30E-27
74	LG:407689.7:2002JAN18	81	152	forward 3	LRR	Leucine Rich Repeat	3.00E-28
74	LG:407689.7:2002JAN18	1191	1913	forward 3	PP2C	Protein phosphatase 2C	3.60E-19
75	LG:407700.1:2002JAN18	338	865	forward 2	PGAM	Phosphoglycerate mutase family	2.10E-08
76	LG:410461.92:2002JAN18	468	764	forward 3	PA	PA domain	2.50E-20
76	LG:410461.92:2002JAN18	993	1115	forward 3	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.30E-05
77	LG:411043.3:2002JAN18	287	1273	forward 2	adh_zinc	Zinc-binding dehydrogenase	1.10E-19
78	LG:438690.47:2002JAN18	550	690	forward 1	zf-CXXC	CXXC zinc finger	1.20E-15
78	LG:438690.47:2002JAN18	1526	1672	forward 2	F-box	F-box domain	2.20E-08
79	LG:444677.81:2002JAN18	652	1092	forward 1	FAA_hydrolase	Fumarylacetoacetate (FAA) hydrolase family	1.30E-29
80	LG:457464.24:2002JAN18	1202	1297	forward 2	zf-RanBP	Zn-finger in Ran binding protein and others	1.50E-11

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
80	LG:457464.24:2002JAN18	795	1034	forward 3	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	1.10E-17
81	LG:7684793.15:2002JAN18	384	512	forward 3	zf-B_box	B-box zinc finger	6.40E-15
81	LG:7684793.15:2002JAN18	183	287	forward 3	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	2.10E-06
82	LG:7687485.1:2002JAN18	46	114	forward 1	zf-C2H2	Zinc finger, C2H2 type	1.00E-50
83	LG:7689661.4:2002JAN18	947	1006	forward 2	zf-C2H2	Zinc finger, C2H2 type	3.90E-44
83	LG:7689661.4:2002JAN18	74	196	forward 2	KRAB	KRAB box	9.60E-24
83	LG:7689661.4:2002JAN18	684	752	forward 3	zf-C2H2	Zinc finger, C2H2 type	5.90E-17
84	LG:7690373.1:2002JAN18	5	73	forward 2	zf-C2H2	Zinc finger, C2H2 type	7.40E-11
85	LG:7696560.1:2002JAN18	966	1064	forward 3	ank	Ankyrin repeat	1.20E-40
86	LG:7698190.26:2002JAN18	105	209	forward 3	SAP	SAP domain	9.30E-10
87	LG:7763560.12:2002JAN18	714	1598	forward 3	NAD_kinase	ATP-NAD kinase	3.90E-51
88	LG:7763587.20:2002JAN18	1979	2077	forward 2	ank	Ankyrin repeat	8.80E-44
89	LG:899263.10:2002JAN18	455	598	forward 2	RCC1	Regulator of chromosome condensation (RCC1)	1.70E-31
90	LG:977837.31:2002JAN18	610	759	forward 1	LRRCT	Leucine rich repeat C-terminal domain	7.00E-09
91	LG:978560.13:2002JAN18	1115	1183	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.80E-93
91	LG:978560.13:2002JAN18	471	593	forward 3	KRAB	KRAB box	9.90E-25
92	LG:979390.2:2002JAN18	85	207	forward 1	KRAB	KRAB box	3.00E-23
93	LG:983019.1:2002JAN18	5	550	forward 2	T-box	T-box	5.80E-106
94	LG:997202.7:2002JAN18	365	529	forward 2	SH3	SH3 domain	4.80E-15
95	LG:998756.3:2002JAN18	454	648	forward 1	zf-DHHC	DHHC zinc finger domain	9.10E-34
96	LG:103460.28:2002JAN18	740	1321	forward 2	UDG	Uracil DNA glycosylase superfamily	1.60E-24
97	LG:1501505.19:2002JAN18	1	429	forward 1	Sulfate_transp	Sulfate transporter family	0.00017
98	LG:233444.9:2002JAN18	85	810	forward 1	DUF300	Domain of unknown function	1.30E-57
98	LG:233444.9:2002JAN18	293	946	forward 2	DUF300	Domain of unknown function	1.70E-39
99	LG:234824.7:2002JAN18	1082	1150	forward 2	LRR	Leucine Rich Repeat	0.00035
99	LG:234824.7:2002JAN18	312	383	forward 3	LRR	Leucine Rich Repeat	1.70E-50
100	LG:235708.23:2002JAN18	15	566	forward 3	DUF300	Domain of unknown function	7.20E-16
101	LG:236649.14:2002JAN18	382	456	forward 1	zf-C2H2	Zinc finger, C2H2 type	0.00021
102	LG:332474.7:2002JAN18	395	469	forward 2	KRAB	KRAB box	0.00046
103	LG:335727.8:2002JAN18	275	391	forward 2	WD40	WD domain, G-beta repeat	4.20E-13

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
104	LG:481983.1:2002JAN18	414	953	forward 3	LAG1	Longevity-assurance protein (LAG1)	1.90E-64

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
10	LG:006394.31:2002JAN18	2653	2730	forward 1	SP	
10	LG:006394.31:2002JAN18	2653	2724	forward 1	SP	
10	LG:006394.31:2002JAN18	2653	2730	forward 1	SP	
10	LG:006394.31:2002JAN18	3539	3628	forward 2	SP	
10	LG:006394.31:2002JAN18	3539	3607	forward 2	SP	
10	LG:006394.31:2002JAN18	2874	2948	forward 3	SP	
11	LG:018258.1:2002JAN18	1	9		TM	Extracellular
11	LG:018258.1:2002JAN18	10	28		TM	Transmembrane
11	LG:018258.1:2002JAN18	29	278		TM	Cytosolic
11	LG:018258.1:2002JAN18	1	222		TM	Cytosolic
11	LG:018258.1:2002JAN18	223	245		TM	Transmembrane
11	LG:018258.1:2002JAN18	246	278		TM	Extracellular
11	LG:018258.1:2002JAN18	26	94	forward 2	SP	
11	LG:018258.1:2002JAN18	26	88	forward 2	SP	
11	LG:018258.1:2002JAN18	26	82	forward 2	SP	
11	LG:018258.1:2002JAN18	636	734	forward 3	SP	
11	LG:018258.1:2002JAN18	663	734	forward 3	SP	
11	LG:018258.1:2002JAN18	636	728	forward 3	SP	
11	LG:018258.1:2002JAN18	663	728	forward 3	SP	
11	LG:018258.1:2002JAN18	663	740	forward 3	SP	
11	LG:018258.1:2002JAN18	663	725	forward 3	SP	
11	LG:018258.1:2002JAN18	663	719	forward 3	SP	
11	LG:018258.1:2002JAN18	663	740	forward 3	SP	
11	LG:018258.1:2002JAN18	663	722	forward 3	SP	
12	LG:027320.5:2002JAN18	1	37		TM	Cytosolic
12	LG:027320.5:2002JAN18	38	60		TM	Transmembrane
12	LG:027320.5:2002JAN18	61	705		TM	Extracellular
12	LG:027320.5:2002JAN18	706	728		TM	Transmembrane
12	LG:027320.5:2002JAN18	729	801		TM	Cytosolic
12	LG:027320.5:2002JAN18	802	824		TM	Transmembrane
12	LG:027320.5:2002JAN18	825	843		TM	Extracellular
12	LG:027320.5:2002JAN18	844	866		TM	Transmembrane
12	LG:027320.5:2002JAN18	867	913		TM	Cytosolic
12	LG:027320.5:2002JAN18	914	936		TM	Transmembrane
12	LG:027320.5:2002JAN18	937	1089		TM	Extracellular
12	LG:027320.5:2002JAN18	1	798		TM	Extracellular
12	LG:027320.5:2002JAN18	799	821		TM	Transmembrane
12	LG:027320.5:2002JAN18	822	833		TM	Cytosolic
12	LG:027320.5:2002JAN18	834	856		TM	Transmembrane
12	LG:027320.5:2002JAN18	857	865		TM	Extracellular
12	LG:027320.5:2002JAN18	866	888		TM	Transmembrane
12	LG:027320.5:2002JAN18	889	1089		TM	Cytosolic
12	LG:027320.5:2002JAN18	1	185		TM	Cytosolic
12	LG:027320.5:2002JAN18	186	208		TM	Transmembrane
12	LG:027320.5:2002JAN18	209	230		TM	Extracellular
12	LG:027320.5:2002JAN18	231	253		TM	Transmembrane
12	LG:027320.5:2002JAN18	254	265		TM	Cytosolic
12	LG:027320.5:2002JAN18	266	288		TM	Transmembrane
12	LG:027320.5:2002JAN18	289	309		TM	Extracellular

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
12	LG:027320.5:2002JAN18	310	332		TM	Transmembrane
12	LG:027320.5:2002JAN18	333	352		TM	Cytosolic
12	LG:027320.5:2002JAN18	353	375		TM	Transmembrane
12	LG:027320.5:2002JAN18	376	378		TM	Extracellular
12	LG:027320.5:2002JAN18	379	401		TM	Transmembrane
12	LG:027320.5:2002JAN18	402	772		TM	Cytosolic
12	LG:027320.5:2002JAN18	773	795		TM	Transmembrane
12	LG:027320.5:2002JAN18	796	799		TM	Extracellular
12	LG:027320.5:2002JAN18	800	822		TM	Transmembrane
12	LG:027320.5:2002JAN18	823	834		TM	Cytosolic
12	LG:027320.5:2002JAN18	835	857		TM	Transmembrane
12	LG:027320.5:2002JAN18	858	1089		TM	Extracellular
12	LG:027320.5:2002JAN18	2386	2439	forward 1	SP	
12	LG:027320.5:2002JAN18	2386	2445	forward 1	SP	
12	LG:027320.5:2002JAN18	1129	1188	forward 1	SP	
12	LG:027320.5:2002JAN18	1129	1191	forward 1	SP	
12	LG:027320.5:2002JAN18	2534	2602	forward 2	SP	
12	LG:027320.5:2002JAN18	810	869	forward 3	SP	
12	LG:027320.5:2002JAN18	810	869	forward 3	SP	
12	LG:027320.5:2002JAN18	729	779	forward 3	SP	
12	LG:027320.5:2002JAN18	810	878	forward 3	SP	
13	LG:057499.1:2002JAN18	1	772		TM	Extracellular
13	LG:057499.1:2002JAN18	773	792		TM	Transmembrane
13	LG:057499.1:2002JAN18	793	804		TM	Cytosolic
13	LG:057499.1:2002JAN18	805	827		TM	Transmembrane
13	LG:057499.1:2002JAN18	828	1209		TM	Extracellular
13	LG:057499.1:2002JAN18	1210	1232		TM	Transmembrane
13	LG:057499.1:2002JAN18	1233	1290		TM	Cytosolic
13	LG:057499.1:2002JAN18	1291	1310		TM	Transmembrane
13	LG:057499.1:2002JAN18	1311	1868		TM	Extracellular
13	LG:057499.1:2002JAN18	1869	1891		TM	Transmembrane
13	LG:057499.1:2002JAN18	1892	1937		TM	Cytosolic
13	LG:057499.1:2002JAN18	1938	1960		TM	Transmembrane
13	LG:057499.1:2002JAN18	1961	2243		TM	Extracellular
13	LG:057499.1:2002JAN18	1	933		TM	Extracellular
13	LG:057499.1:2002JAN18	934	956		TM	Transmembrane
13	LG:057499.1:2002JAN18	957	1177		TM	Cytosolic
13	LG:057499.1:2002JAN18	1178	1200		TM	Transmembrane
13	LG:057499.1:2002JAN18	1201	1209		TM	Extracellular
13	LG:057499.1:2002JAN18	1210	1232		TM	Transmembrane
13	LG:057499.1:2002JAN18	1233	1345		TM	Cytosolic
13	LG:057499.1:2002JAN18	1346	1368		TM	Transmembrane
13	LG:057499.1:2002JAN18	1369	1387		TM	Extracellular
13	LG:057499.1:2002JAN18	1388	1410		TM	Transmembrane
13	LG:057499.1:2002JAN18	1411	1429		TM	Cytosolic
13	LG:057499.1:2002JAN18	1430	1452		TM	Transmembrane
13	LG:057499.1:2002JAN18	1453	1937		TM	Extracellular
13	LG:057499.1:2002JAN18	1938	1960		TM	Transmembrane
13	LG:057499.1:2002JAN18	1961	2098		TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
13	LG:057499.1:2002JAN18	2099	2121		TM	Transmembrane
13	LG:057499.1:2002JAN18	2122	2140		TM	Extracellular
13	LG:057499.1:2002JAN18	2141	2163		TM	Transmembrane
13	LG:057499.1:2002JAN18	2164	2169		TM	Cytosolic
13	LG:057499.1:2002JAN18	2170	2192		TM	Transmembrane
13	LG:057499.1:2002JAN18	2193	2243		TM	Extracellular
13	LG:057499.1:2002JAN18	1	771		TM	Extracellular
13	LG:057499.1:2002JAN18	772	793		TM	Transmembrane
13	LG:057499.1:2002JAN18	794	958		TM	Cytosolic
13	LG:057499.1:2002JAN18	959	981		TM	Transmembrane
13	LG:057499.1:2002JAN18	982	1084		TM	Extracellular
13	LG:057499.1:2002JAN18	1085	1107		TM	Transmembrane
13	LG:057499.1:2002JAN18	1108	1200		TM	Cytosolic
13	LG:057499.1:2002JAN18	1201	1223		TM	Transmembrane
13	LG:057499.1:2002JAN18	1224	1303		TM	Extracellular
13	LG:057499.1:2002JAN18	1304	1326		TM	Transmembrane
13	LG:057499.1:2002JAN18	1327	1422		TM	Cytosolic
13	LG:057499.1:2002JAN18	1423	1445		TM	Transmembrane
13	LG:057499.1:2002JAN18	1446	1482		TM	Extracellular
13	LG:057499.1:2002JAN18	1483	1505		TM	Transmembrane
13	LG:057499.1:2002JAN18	1506	1593		TM	Cytosolic
13	LG:057499.1:2002JAN18	1594	1613		TM	Transmembrane
13	LG:057499.1:2002JAN18	1614	1627		TM	Extracellular
13	LG:057499.1:2002JAN18	1628	1650		TM	Transmembrane
13	LG:057499.1:2002JAN18	1651	1656		TM	Cytosolic
13	LG:057499.1:2002JAN18	1657	1679		TM	Transmembrane
13	LG:057499.1:2002JAN18	1680	1683		TM	Extracellular
13	LG:057499.1:2002JAN18	1684	1706		TM	Transmembrane
13	LG:057499.1:2002JAN18	1707	1799		TM	Cytosolic
13	LG:057499.1:2002JAN18	1800	1822		TM	Transmembrane
13	LG:057499.1:2002JAN18	1823	1936		TM	Extracellular
13	LG:057499.1:2002JAN18	1937	1959		TM	Transmembrane
13	LG:057499.1:2002JAN18	1960	2097		TM	Cytosolic
13	LG:057499.1:2002JAN18	2098	2120		TM	Transmembrane
13	LG:057499.1:2002JAN18	2121	2151		TM	Extracellular
13	LG:057499.1:2002JAN18	2152	2174		TM	Transmembrane
13	LG:057499.1:2002JAN18	2175	2242		TM	Cytosolic
13	LG:057499.1:2002JAN18	5782	5859	forward 1	SP	
13	LG:057499.1:2002JAN18	2329	2400	forward 1	SP	
13	LG:057499.1:2002JAN18	2329	2400	forward 1	SP	
13	LG:057499.1:2002JAN18	2329	2379	forward 1	SP	
13	LG:057499.1:2002JAN18	5809	5859	forward 1	SP	
13	LG:057499.1:2002JAN18	5809	5868	forward 1	SP	
13	LG:057499.1:2002JAN18	6303	6374	forward 3	SP	
13	LG:057499.1:2002JAN18	6297	6374	forward 3	SP	
13	LG:057499.1:2002JAN18	6312	6368	forward 3	SP	
13	LG:057499.1:2002JAN18	6294	6368	forward 3	SP	
13	LG:057499.1:2002JAN18	6303	6368	forward 3	SP	
13	LG:057499.1:2002JAN18	6312	6371	forward 3	SP	

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
14	LG:065935.21:2002JAN18	1	166		TM	Extracellular
14	LG:065935.21:2002JAN18	167	189		TM	Transmembrane
14	LG:065935.21:2002JAN18	190	201		TM	Cytosolic
14	LG:065935.21:2002JAN18	202	224		TM	Transmembrane
14	LG:065935.21:2002JAN18	225	313		TM	Extracellular
15	LG:071860.12:2002JAN18	1	49		TM	Extracellular
15	LG:071860.12:2002JAN18	50	72		TM	Transmembrane
15	LG:071860.12:2002JAN18	73	117		TM	Cytosolic
15	LG:071860.12:2002JAN18	118	140		TM	Transmembrane
15	LG:071860.12:2002JAN18	141	257		TM	Extracellular
15	LG:071860.12:2002JAN18	240	308	forward 3	SP	
15	LG:071860.12:2002JAN18	240	314	forward 3	SP	
15	LG:071860.12:2002JAN18	240	314	forward 3	SP	
15	LG:071860.12:2002JAN18	240	317	forward 3	SP	
15	LG:071860.12:2002JAN18	240	320	forward 3	SP	
16	LG:087383.29:2002JAN18	1103	1165	forward 2	SP	
16	LG:087383.29:2002JAN18	1100	1153	forward 2	SP	
16	LG:087383.29:2002JAN18	1103	1165	forward 2	SP	
17	LG:098580.3:2002JAN18	1	161		TM	Extracellular
17	LG:098580.3:2002JAN18	162	184		TM	Transmembrane
17	LG:098580.3:2002JAN18	185	221		TM	Cytosolic
17	LG:098580.3:2002JAN18	222	244		TM	Transmembrane
17	LG:098580.3:2002JAN18	245	250		TM	Extracellular
17	LG:098580.3:2002JAN18	1	168		TM	Cytosolic
17	LG:098580.3:2002JAN18	169	191		TM	Transmembrane
17	LG:098580.3:2002JAN18	192	222		TM	Extracellular
17	LG:098580.3:2002JAN18	223	245		TM	Transmembrane
17	LG:098580.3:2002JAN18	246	250		TM	Cytosolic
17	LG:098580.3:2002JAN18	1	219		TM	Cytosolic
17	LG:098580.3:2002JAN18	220	242		TM	Transmembrane
17	LG:098580.3:2002JAN18	243	250		TM	Extracellular
17	LG:098580.3:2002JAN18	504	569	forward 3	SP	
18	LG:1001879.1:2002JAN18	148	225	forward 1	SP	
18	LG:1001879.1:2002JAN18	148	225	forward 1	SP	
18	LG:1001879.1:2002JAN18	148	225	forward 1	SP	
18	LG:1001879.1:2002JAN18	148	219	forward 1	SP	
18	LG:1001879.1:2002JAN18	148	207	forward 1	SP	
18	LG:1001879.1:2002JAN18	148	219	forward 1	SP	
18	LG:1001879.1:2002JAN18	148	225	forward 1	SP	
18	LG:1001879.1:2002JAN18	148	210	forward 1	SP	
18	LG:1001879.1:2002JAN18	148	204	forward 1	SP	
19	LG:1079456.4:2002JAN18	1	218		TM	Extracellular
19	LG:1079456.4:2002JAN18	219	241		TM	Transmembrane
19	LG:1079456.4:2002JAN18	242	256		TM	Cytosolic
19	LG:1079456.4:2002JAN18	548	625	forward 2	SP	
19	LG:1079456.4:2002JAN18	548	625	forward 2	SP	
19	LG:1079456.4:2002JAN18	548	619	forward 2	SP	
19	LG:1079456.4:2002JAN18	548	601	forward 2	SP	
19	LG:1079456.4:2002JAN18	548	625	forward 2	SP	

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
19	LG:1079456.4:2002JAN18	548	613	forward 2	SP	
19	LG:1079456.4:2002JAN18	548	610	forward 2	SP	
19	LG:1079456.4:2002JAN18	548	610	forward 2	SP	
19	LG:1079456.4:2002JAN18	548	619	forward 2	SP	
20	LG:1080598.9:2002JAN18	182	238	forward 2	SP	
21	LG:1090358.10:2002JAN18	1	3		TM	Extracellular
21	LG:1090358.10:2002JAN18	4	26		TM	Transmembrane
21	LG:1090358.10:2002JAN18	27	30		TM	Cytosolic
21	LG:1090358.10:2002JAN18	31	53		TM	Transmembrane
21	LG:1090358.10:2002JAN18	54	733		TM	Extracellular
21	LG:1090358.10:2002JAN18	1	3		TM	Extracellular
21	LG:1090358.10:2002JAN18	4	26		TM	Transmembrane
21	LG:1090358.10:2002JAN18	27	32		TM	Cytosolic
21	LG:1090358.10:2002JAN18	33	55		TM	Transmembrane
21	LG:1090358.10:2002JAN18	56	733		TM	Extracellular
21	LG:1090358.10:2002JAN18	1226	1285	forward 2	SP	
21	LG:1090358.10:2002JAN18	1226	1276	forward 2	SP	
21	LG:1090358.10:2002JAN18	1226	1288	forward 2	SP	
21	LG:1090358.10:2002JAN18	1226	1291	forward 2	SP	
21	LG:1090358.10:2002JAN18	692	757	forward 2	SP	
22	LG:1097492.2:2002JAN18	2941	3012	forward 1	SP	
22	LG:1097492.2:2002JAN18	2941	3012	forward 1	SP	
22	LG:1097492.2:2002JAN18	2941	3012	forward 1	SP	
22	LG:1097492.2:2002JAN18	2941	3006	forward 1	SP	
22	LG:1097492.2:2002JAN18	539	634	forward 2	SP	
22	LG:1097492.2:2002JAN18	2331	2402	forward 3	SP	
22	LG:1097492.2:2002JAN18	2331	2408	forward 3	SP	
22	LG:1097492.2:2002JAN18	2331	2426	forward 3	SP	
22	LG:1097492.2:2002JAN18	2331	2402	forward 3	SP	
22	LG:1097492.2:2002JAN18	2331	2396	forward 3	SP	
22	LG:1097492.2:2002JAN18	2331	2393	forward 3	SP	
22	LG:1097492.2:2002JAN18	2331	2402	forward 3	SP	
23	LG:1099945.26:2002JAN18	1	726		TM	Extracellular
23	LG:1099945.26:2002JAN18	727	744		TM	Transmembrane
23	LG:1099945.26:2002JAN18	745	842		TM	Cytosolic
23	LG:1099945.26:2002JAN18	1738	1809	forward 1	SP	
24	LG:110016.1:2002JAN18	1762	1857	forward 1	SP	
24	LG:110016.1:2002JAN18	154	258	forward 1	SP	
24	LG:110016.1:2002JAN18	740	826	forward 2	SP	
24	LG:110016.1:2002JAN18	953	1012	forward 2	SP	
24	LG:110016.1:2002JAN18	1344	1421	forward 3	SP	
24	LG:110016.1:2002JAN18	1344	1421	forward 3	SP	
25	LG:1137613.10:2002JAN18	1	874		TM	Extracellular
25	LG:1137613.10:2002JAN18	875	897		TM	Transmembrane
25	LG:1137613.10:2002JAN18	898	903		TM	Cytosolic
25	LG:1137613.10:2002JAN18	1	363		TM	Extracellular
25	LG:1137613.10:2002JAN18	364	386		TM	Transmembrane
25	LG:1137613.10:2002JAN18	387	398		TM	Cytosolic
25	LG:1137613.10:2002JAN18	399	421		TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
25	LG:1137613.10:2002JAN18	422	903		TM	Extracellular
25	LG:1137613.10:2002JAN18	1	213		TM	Extracellular
25	LG:1137613.10:2002JAN18	214	236		TM	Transmembrane
25	LG:1137613.10:2002JAN18	237	394		TM	Cytosolic
25	LG:1137613.10:2002JAN18	395	417		TM	Transmembrane
25	LG:1137613.10:2002JAN18	418	458		TM	Extracellular
25	LG:1137613.10:2002JAN18	459	481		TM	Transmembrane
25	LG:1137613.10:2002JAN18	482	665		TM	Cytosolic
25	LG:1137613.10:2002JAN18	666	688		TM	Transmembrane
25	LG:1137613.10:2002JAN18	689	903		TM	Extracellular
25	LG:1137613.10:2002JAN18	2647	2706	forward 1	SP	
25	LG:1137613.10:2002JAN18	2647	2706	forward 1	SP	
25	LG:1137613.10:2002JAN18	2647	2703	forward 1	SP	
25	LG:1137613.10:2002JAN18	2647	2700	forward 1	SP	
25	LG:1137613.10:2002JAN18	1028	1087	forward 2	SP	
25	LG:1137613.10:2002JAN18	1172	1258	forward 2	SP	
25	LG:1137613.10:2002JAN18	1028	1087	forward 2	SP	
25	LG:1137613.10:2002JAN18	1566	1655	forward 3	SP	
25	LG:1137613.10:2002JAN18	1371	1439	forward 3	SP	
25	LG:1137613.10:2002JAN18	1371	1430	forward 3	SP	
25	LG:1137613.10:2002JAN18	1371	1436	forward 3	SP	
26	LG:118836.26:2002JAN18	3778	3855	forward 1	SP	
26	LG:118836.26:2002JAN18	1529	1618	forward 2	SP	
26	LG:118836.26:2002JAN18	1529	1606	forward 2	SP	
26	LG:118836.26:2002JAN18	1529	1600	forward 2	SP	
26	LG:118836.26:2002JAN18	4940	5002	forward 2	SP	
26	LG:118836.26:2002JAN18	1529	1600	forward 2	SP	
26	LG:118836.26:2002JAN18	3791	3850	forward 2	SP	
26	LG:118836.26:2002JAN18	756	830	forward 3	SP	
26	LG:118836.26:2002JAN18	756	809	forward 3	SP	
26	LG:118836.26:2002JAN18	756	821	forward 3	SP	
26	LG:118836.26:2002JAN18	756	818	forward 3	SP	
26	LG:118836.26:2002JAN18	756	815	forward 3	SP	
26	LG:118836.26:2002JAN18	756	815	forward 3	SP	
27	LG:1330261.32:2002JAN18	1	284		TM	Extracellular
27	LG:1330261.32:2002JAN18	285	307		TM	Transmembrane
27	LG:1330261.32:2002JAN18	308	460		TM	Cytosolic
27	LG:1330261.32:2002JAN18	461	483		TM	Transmembrane
27	LG:1330261.32:2002JAN18	484	511		TM	Extracellular
27	LG:1330261.32:2002JAN18	512	534		TM	Transmembrane
27	LG:1330261.32:2002JAN18	535	559		TM	Cytosolic
27	LG:1330261.32:2002JAN18	560	582		TM	Transmembrane
27	LG:1330261.32:2002JAN18	583	616		TM	Extracellular
27	LG:1330261.32:2002JAN18	617	639		TM	Transmembrane
27	LG:1330261.32:2002JAN18	640	645		TM	Cytosolic
27	LG:1330261.32:2002JAN18	646	668		TM	Transmembrane
27	LG:1330261.32:2002JAN18	669	726		TM	Extracellular
27	LG:1330261.32:2002JAN18	727	749		TM	Transmembrane
27	LG:1330261.32:2002JAN18	750	761		TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
27	LG:1330261.32:2002JAN18	762	784		TM	Transmembrane
27	LG:1330261.32:2002JAN18	785	2007		TM	Extracellular
27	LG:1330261.32:2002JAN18	2245	2325	forward 1	SP	
27	LG:1330261.32:2002JAN18	865	927	forward 1	SP	
27	LG:1330261.32:2002JAN18	2245	2325	forward 1	SP	
27	LG:1330261.32:2002JAN18	4987	5046	forward 1	SP	
27	LG:1330261.32:2002JAN18	2245	2325	forward 1	SP	
27	LG:1330261.32:2002JAN18	5104	5199	forward 1	SP	
27	LG:1330261.32:2002JAN18	1085	1144	forward 2	SP	
27	LG:1330261.32:2002JAN18	2153	2251	forward 2	SP	
27	LG:1330261.32:2002JAN18	2153	2218	forward 2	SP	
27	LG:1330261.32:2002JAN18	1052	1108	forward 2	SP	
27	LG:1330261.32:2002JAN18	1052	1126	forward 2	SP	
27	LG:1330261.32:2002JAN18	1052	1120	forward 2	SP	
28	LG:1347461.28:2002JAN18	1	1051		TM	Extracellular
28	LG:1347461.28:2002JAN18	1052	1074		TM	Transmembrane
28	LG:1347461.28:2002JAN18	1075	1085		TM	Cytosolic
28	LG:1347461.28:2002JAN18	1086	1105		TM	Transmembrane
28	LG:1347461.28:2002JAN18	1106	1150		TM	Extracellular
28	LG:1347461.28:2002JAN18	1151	1173		TM	Transmembrane
28	LG:1347461.28:2002JAN18	1174	1282		TM	Cytosolic
28	LG:1347461.28:2002JAN18	1283	1305		TM	Transmembrane
28	LG:1347461.28:2002JAN18	1306	1331		TM	Extracellular
28	LG:1347461.28:2002JAN18	364	414	forward 1	SP	
29	LG:1383494.16:2002JAN18	1	579		TM	Extracellular
29	LG:1383494.16:2002JAN18	580	602		TM	Transmembrane
29	LG:1383494.16:2002JAN18	603	712		TM	Cytosolic
29	LG:1383494.16:2002JAN18	713	735		TM	Transmembrane
29	LG:1383494.16:2002JAN18	736	962		TM	Extracellular
29	LG:1383494.16:2002JAN18	963	985		TM	Transmembrane
29	LG:1383494.16:2002JAN18	986	1048		TM	Cytosolic
29	LG:1383494.16:2002JAN18	1049	1071		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1072	1080		TM	Extracellular
29	LG:1383494.16:2002JAN18	1081	1103		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1104	1239		TM	Cytosolic
29	LG:1383494.16:2002JAN18	1240	1262		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1263	1276		TM	Extracellular
29	LG:1383494.16:2002JAN18	1277	1299		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1300	1441		TM	Cytosolic
29	LG:1383494.16:2002JAN18	1442	1464		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1465	1535		TM	Extracellular
29	LG:1383494.16:2002JAN18	1536	1558		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1559	1771		TM	Cytosolic
29	LG:1383494.16:2002JAN18	1772	1794		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1795	1800		TM	Extracellular
29	LG:1383494.16:2002JAN18	1	1049		TM	Extracellular
29	LG:1383494.16:2002JAN18	1050	1072		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1073	1073		TM	Cytosolic
29	LG:1383494.16:2002JAN18	1074	1096		TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
29	LG:1383494.16:2002JAN18	1097	1115		TM	Extracellular
29	LG:1383494.16:2002JAN18	1116	1138		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1139	1144		TM	Cytosolic
29	LG:1383494.16:2002JAN18	1145	1164		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1165	1253		TM	Extracellular
29	LG:1383494.16:2002JAN18	1254	1276		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1277	1282		TM	Cytosolic
29	LG:1383494.16:2002JAN18	1283	1305		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1306	1533		TM	Extracellular
29	LG:1383494.16:2002JAN18	1534	1556		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1557	1800		TM	Cytosolic
29	LG:1383494.16:2002JAN18	1	263		TM	Cytosolic
29	LG:1383494.16:2002JAN18	264	286		TM	Transmembrane
29	LG:1383494.16:2002JAN18	287	690		TM	Extracellular
29	LG:1383494.16:2002JAN18	691	709		TM	Transmembrane
29	LG:1383494.16:2002JAN18	710	721		TM	Cytosolic
29	LG:1383494.16:2002JAN18	722	744		TM	Transmembrane
29	LG:1383494.16:2002JAN18	745	785		TM	Extracellular
29	LG:1383494.16:2002JAN18	786	808		TM	Transmembrane
29	LG:1383494.16:2002JAN18	809	957		TM	Cytosolic
29	LG:1383494.16:2002JAN18	958	980		TM	Transmembrane
29	LG:1383494.16:2002JAN18	981	983		TM	Extracellular
29	LG:1383494.16:2002JAN18	984	1003		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1004	1046		TM	Cytosolic
29	LG:1383494.16:2002JAN18	1047	1069		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1070	1078		TM	Extracellular
29	LG:1383494.16:2002JAN18	1079	1101		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1102	1121		TM	Cytosolic
29	LG:1383494.16:2002JAN18	1122	1144		TM	Transmembrane
29	LG:1383494.16:2002JAN18	1145	1799		TM	Extracellular
29	LG:1383494.16:2002JAN18	139	225	forward 1	SP	
29	LG:1383494.16:2002JAN18	139	225	forward 1	SP	
29	LG:1383494.16:2002JAN18	139	219	forward 1	SP	
29	LG:1383494.16:2002JAN18	139	210	forward 1	SP	
29	LG:1383494.16:2002JAN18	139	213	forward 1	SP	
29	LG:1383494.16:2002JAN18	139	207	forward 1	SP	
29	LG:1383494.16:2002JAN18	139	198	forward 1	SP	
29	LG:1383494.16:2002JAN18	145	207	forward 1	SP	
29	LG:1383494.16:2002JAN18	4595	4648	forward 2	SP	
29	LG:1383494.16:2002JAN18	4595	4654	forward 2	SP	
29	LG:1383494.16:2002JAN18	4595	4651	forward 2	SP	
29	LG:1383494.16:2002JAN18	1692	1751	forward 3	SP	
29	LG:1383494.16:2002JAN18	1692	1754	forward 3	SP	
30	LG:1400155.1:2002JAN18	1	1563		TM	Extracellular
30	LG:1400155.1:2002JAN18	1564	1586		TM	Transmembrane
30	LG:1400155.1:2002JAN18	1587	1644		TM	Cytosolic
30	LG:1400155.1:2002JAN18	1	1041		TM	Extracellular
30	LG:1400155.1:2002JAN18	1042	1064		TM	Transmembrane
30	LG:1400155.1:2002JAN18	1065	1201		TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
30	LG:1400155.1:2002JAN18	1202	1224		TM	Transmembrane
30	LG:1400155.1:2002JAN18	1225	1489		TM	Extracellular
30	LG:1400155.1:2002JAN18	1490	1512		TM	Transmembrane
30	LG:1400155.1:2002JAN18	1513	1558		TM	Cytosolic
30	LG:1400155.1:2002JAN18	1559	1581		TM	Transmembrane
30	LG:1400155.1:2002JAN18	1582	1595		TM	Extracellular
30	LG:1400155.1:2002JAN18	1596	1618		TM	Transmembrane
30	LG:1400155.1:2002JAN18	1619	1644		TM	Cytosolic
30	LG:1400155.1:2002JAN18	1	1475		TM	Extracellular
30	LG:1400155.1:2002JAN18	1476	1498		TM	Transmembrane
30	LG:1400155.1:2002JAN18	1499	1552		TM	Cytosolic
30	LG:1400155.1:2002JAN18	1553	1575		TM	Transmembrane
30	LG:1400155.1:2002JAN18	1576	1604		TM	Extracellular
30	LG:1400155.1:2002JAN18	1605	1624		TM	Transmembrane
30	LG:1400155.1:2002JAN18	1625	1643		TM	Cytosolic
30	LG:1400155.1:2002JAN18	2168	2245	forward 2	SP	
30	LG:1400155.1:2002JAN18	2168	2245	forward 2	SP	
30	LG:1400155.1:2002JAN18	2339	2443	forward 2	SP	
30	LG:1400155.1:2002JAN18	2168	2242	forward 2	SP	
30	LG:1400155.1:2002JAN18	2187	2255	forward 3	SP	
30	LG:1400155.1:2002JAN18	2187	2249	forward 3	SP	
30	LG:1400155.1:2002JAN18	2187	2261	forward 3	SP	
30	LG:1400155.1:2002JAN18	2187	2267	forward 3	SP	
30	LG:1400155.1:2002JAN18	2187	2240	forward 3	SP	
31	LG:1446621.1:2002JAN18	1	19		TM	Cytosolic
31	LG:1446621.1:2002JAN18	20	42		TM	Transmembrane
31	LG:1446621.1:2002JAN18	43	353		TM	Extracellular
32	LG:144920.1:2002JAN18	1376	1432	forward 2	SP	
32	LG:144920.1:2002JAN18	1376	1438	forward 2	SP	
32	LG:144920.1:2002JAN18	1376	1435	forward 2	SP	
33	LG:1452619.1:2002JAN18	1	6		TM	Cytosolic
33	LG:1452619.1:2002JAN18	7	29		TM	Transmembrane
33	LG:1452619.1:2002JAN18	30	591		TM	Extracellular
33	LG:1452619.1:2002JAN18	592	614		TM	Transmembrane
33	LG:1452619.1:2002JAN18	615	806		TM	Cytosolic
33	LG:1452619.1:2002JAN18	807	829		TM	Transmembrane
33	LG:1452619.1:2002JAN18	830	838		TM	Extracellular
33	LG:1452619.1:2002JAN18	839	861		TM	Transmembrane
33	LG:1452619.1:2002JAN18	862	872		TM	Cytosolic
33	LG:1452619.1:2002JAN18	873	895		TM	Transmembrane
33	LG:1452619.1:2002JAN18	896	1275		TM	Extracellular
33	LG:1452619.1:2002JAN18	1276	1295		TM	Transmembrane
33	LG:1452619.1:2002JAN18	1296	1323		TM	Cytosolic
33	LG:1452619.1:2002JAN18	1324	1346		TM	Transmembrane
33	LG:1452619.1:2002JAN18	1347	1392		TM	Extracellular
33	LG:1452619.1:2002JAN18	1393	1412		TM	Transmembrane
33	LG:1452619.1:2002JAN18	1413	1588		TM	Cytosolic
33	LG:1452619.1:2002JAN18	1	589		TM	Extracellular
33	LG:1452619.1:2002JAN18	590	612		TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
33	LG:1452619.1:2002JAN18	613	803		TM	Cytosolic
33	LG:1452619.1:2002JAN18	804	826		TM	Transmembrane
33	LG:1452619.1:2002JAN18	827	835		TM	Extracellular
33	LG:1452619.1:2002JAN18	836	858		TM	Transmembrane
33	LG:1452619.1:2002JAN18	859	1329		TM	Cytosolic
33	LG:1452619.1:2002JAN18	1330	1352		TM	Transmembrane
33	LG:1452619.1:2002JAN18	1353	1388		TM	Extracellular
33	LG:1452619.1:2002JAN18	1389	1411		TM	Transmembrane
33	LG:1452619.1:2002JAN18	1412	1417		TM	Cytosolic
33	LG:1452619.1:2002JAN18	1418	1437		TM	Transmembrane
33	LG:1452619.1:2002JAN18	1438	1506		TM	Extracellular
33	LG:1452619.1:2002JAN18	1507	1526		TM	Transmembrane
33	LG:1452619.1:2002JAN18	1527	1587		TM	Cytosolic
33	LG:1452619.1:2002JAN18	1	588		TM	Extracellular
33	LG:1452619.1:2002JAN18	589	611		TM	Transmembrane
33	LG:1452619.1:2002JAN18	612	647		TM	Cytosolic
33	LG:1452619.1:2002JAN18	648	670		TM	Transmembrane
33	LG:1452619.1:2002JAN18	671	679		TM	Extracellular
33	LG:1452619.1:2002JAN18	680	697		TM	Transmembrane
33	LG:1452619.1:2002JAN18	698	759		TM	Cytosolic
33	LG:1452619.1:2002JAN18	760	782		TM	Transmembrane
33	LG:1452619.1:2002JAN18	783	801		TM	Extracellular
33	LG:1452619.1:2002JAN18	802	824		TM	Transmembrane
33	LG:1452619.1:2002JAN18	825	1270		TM	Cytosolic
33	LG:1452619.1:2002JAN18	1271	1293		TM	Transmembrane
33	LG:1452619.1:2002JAN18	1294	1296		TM	Extracellular
33	LG:1452619.1:2002JAN18	1297	1314		TM	Transmembrane
33	LG:1452619.1:2002JAN18	1315	1330		TM	Cytosolic
33	LG:1452619.1:2002JAN18	1331	1353		TM	Transmembrane
33	LG:1452619.1:2002JAN18	1354	1476		TM	Extracellular
33	LG:1452619.1:2002JAN18	1477	1499		TM	Transmembrane
33	LG:1452619.1:2002JAN18	1500	1587		TM	Cytosolic
33	LG:1452619.1:2002JAN18	1780	1851	forward 1	SP	
33	LG:1452619.1:2002JAN18	3805	3888	forward 1	SP	
33	LG:1452619.1:2002JAN18	3043	3099	forward 1	SP	
33	LG:1452619.1:2002JAN18	902	946	forward 2	SP	
33	LG:1452619.1:2002JAN18	902	952	forward 2	SP	
33	LG:1452619.1:2002JAN18	902	964	forward 2	SP	
33	LG:1452619.1:2002JAN18	884	955	forward 2	SP	
33	LG:1452619.1:2002JAN18	2111	2176	forward 2	SP	
33	LG:1452619.1:2002JAN18	884	982	forward 2	SP	
33	LG:1452619.1:2002JAN18	902	982	forward 2	SP	
33	LG:1452619.1:2002JAN18	2274	2342	forward 3	SP	
33	LG:1452619.1:2002JAN18	2253	2342	forward 3	SP	
34	LG:1453417.6:2002JAN18	1	2453		TM	Extracellular
34	LG:1453417.6:2002JAN18	2454	2476		TM	Transmembrane
34	LG:1453417.6:2002JAN18	2477	2488		TM	Cytosolic
34	LG:1453417.6:2002JAN18	2489	2508		TM	Transmembrane
34	LG:1453417.6:2002JAN18	2509	2511		TM	Extracellular

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
34	LG:1453417.6:2002JAN18,	2512	2534		TM	Transmembrane
34	LG:1453417.6:2002JAN18	2535	2554		TM	Cytosolic
34	LG:1453417.6:2002JAN18	2555	2574		TM	Transmembrane
34	LG:1453417.6:2002JAN18	2575	2593		TM	Extracellular
34	LG:1453417.6:2002JAN18	2594	2616		TM	Transmembrane
34	LG:1453417.6:2002JAN18	2617	2635		TM	Cytosolic
34	LG:1453417.6:2002JAN18	2636	2658		TM	Transmembrane
34	LG:1453417.6:2002JAN18	2659	3378		TM	Extracellular
34	LG:1453417.6:2002JAN18	3379	3401		TM	Transmembrane
34	LG:1453417.6:2002JAN18	3402	3533		TM	Cytosolic
34	LG:1453417.6:2002JAN18	3534	3556		TM	Transmembrane
34	LG:1453417.6:2002JAN18	3557	3564		TM	Extracellular
34	LG:1453417.6:2002JAN18	1	3534		TM	Extracellular
34	LG:1453417.6:2002JAN18	3535	3557		TM	Transmembrane
34	LG:1453417.6:2002JAN18	3558	3564		TM	Cytosolic
34	LG:1453417.6:2002JAN18	223	324	forward 1	SP	
34	LG:1453417.6:2002JAN18	247	324	forward 1	SP	
34	LG:1453417.6:2002JAN18	259	321	forward 1	SP	
34	LG:1453417.6:2002JAN18	265	318	forward 1	SP	
34	LG:1453417.6:2002JAN18	265	324	forward 1	SP	
34	LG:1453417.6:2002JAN18	7675	7722	forward 1	SP	
34	LG:1453417.6:2002JAN18	5108	5215	forward 2	SP	
34	LG:1453417.6:2002JAN18	4172	4237	forward 2	SP	
34	LG:1453417.6:2002JAN18	7643	7717	forward 2	SP	
34	LG:1453417.6:2002JAN18	7643	7717	forward 2	SP	
34	LG:1453417.6:2002JAN18	5567	5626	forward 2	SP	
34	LG:1453417.6:2002JAN18	7643	7702	forward 2	SP	
34	LG:1453417.6:2002JAN18	1803	1856	forward 3	SP	
35	LG:148485.8:2002JAN18	1	694		TM	Extracellular
35	LG:148485.8:2002JAN18	695	717		TM	Transmembrane
35	LG:148485.8:2002JAN18	718	801		TM	Cytosolic
35	LG:148485.8:2002JAN18	802	824		TM	Transmembrane
35	LG:148485.8:2002JAN18	825	838		TM	Extracellular
35	LG:148485.8:2002JAN18	839	861		TM	Transmembrane
35	LG:148485.8:2002JAN18	862	941		TM	Cytosolic
35	LG:148485.8:2002JAN18	942	964		TM	Transmembrane
35	LG:148485.8:2002JAN18	965	967		TM	Extracellular
35	LG:148485.8:2002JAN18	968	990		TM	Transmembrane
35	LG:148485.8:2002JAN18	991	1069		TM	Cytosolic
35	LG:148485.8:2002JAN18	1070	1089		TM	Transmembrane
35	LG:148485.8:2002JAN18	1090	1114		TM	Extracellular
35	LG:148485.8:2002JAN18	1	20		TM	Cytosolic
35	LG:148485.8:2002JAN18	21	39		TM	Transmembrane
35	LG:148485.8:2002JAN18	40	53		TM	Extracellular
35	LG:148485.8:2002JAN18	54	76		TM	Transmembrane
35	LG:148485.8:2002JAN18	77	192		TM	Cytosolic
35	LG:148485.8:2002JAN18	193	215		TM	Transmembrane
35	LG:148485.8:2002JAN18	216	622		TM	Extracellular
35	LG:148485.8:2002JAN18	623	645		TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
35	LG:148485.8:2002JAN18	646	794		TM	Cytosolic
35	LG:148485.8:2002JAN18	795	817		TM	Transmembrane
35	LG:148485.8:2002JAN18	818	845		TM	Extracellular
35	LG:148485.8:2002JAN18	846	868		TM	Transmembrane
35	LG:148485.8:2002JAN18	869	1045		TM	Cytosolic
35	LG:148485.8:2002JAN18	1046	1065		TM	Transmembrane
35	LG:148485.8:2002JAN18	1066	1074		TM	Extracellular
35	LG:148485.8:2002JAN18	1075	1097		TM	Transmembrane
35	LG:148485.8:2002JAN18	1098	1114		TM	Cytosolic
35	LG:148485.8:2002JAN18	1	799		TM	Extracellular
35	LG:148485.8:2002JAN18	800	822		TM	Transmembrane
35	LG:148485.8:2002JAN18	823	834		TM	Cytosolic
35	LG:148485.8:2002JAN18	835	857		TM	Transmembrane
35	LG:148485.8:2002JAN18	858	946		TM	Extracellular
35	LG:148485.8:2002JAN18	947	969		TM	Transmembrane
35	LG:148485.8:2002JAN18	970	980		TM	Cytosolic
35	LG:148485.8:2002JAN18	981	1003		TM	Transmembrane
35	LG:148485.8:2002JAN18	1004	1042		TM	Extracellular
35	LG:148485.8:2002JAN18	1043	1065		TM	Transmembrane
35	LG:148485.8:2002JAN18	1066	1113		TM	Cytosolic
35	LG:148485.8:2002JAN18	2381	2452	forward 2	SP	
35	LG:148485.8:2002JAN18	1373	1465	forward 2	SP	
35	LG:148485.8:2002JAN18	1373	1474	forward 2	SP	
35	LG:148485.8:2002JAN18	2381	2446	forward 2	SP	
36	LG:1502670.1:2002JAN18	293	376	forward 2	SP	
36	LG:1502670.1:2002JAN18	293	382	forward 2	SP	
36	LG:1502670.1:2002JAN18	293	364	forward 2	SP	
36	LG:1502670.1:2002JAN18	293	382	forward 2	SP	
37	LG:206593.3:2002JAN18	1	464		TM	Extracellular
37	LG:206593.3:2002JAN18	465	484		TM	Transmembrane
37	LG:206593.3:2002JAN18	485	516		TM	Cytosolic
37	LG:206593.3:2002JAN18	1364	1462	forward 2	SP	
38	LG:228273.22:2002JAN18	1	924		TM	Extracellular
38	LG:228273.22:2002JAN18	925	947		TM	Transmembrane
38	LG:228273.22:2002JAN18	948	959		TM	Cytosolic
38	LG:228273.22:2002JAN18	960	982		TM	Transmembrane
38	LG:228273.22:2002JAN18	983	1804		TM	Extracellular
38	LG:228273.22:2002JAN18	1	1643		TM	Extracellular
38	LG:228273.22:2002JAN18	1644	1666		TM	Transmembrane
38	LG:228273.22:2002JAN18	1667	1803		TM	Cytosolic
38	LG:228273.22:2002JAN18	2863	2949	forward 1	SP	
38	LG:228273.22:2002JAN18	3875	3934	forward 2	SP	
39	LG:228319.2:2002JAN18	1	305		TM	Extracellular
39	LG:228319.2:2002JAN18	306	328		TM	Transmembrane
39	LG:228319.2:2002JAN18	329	410		TM	Cytosolic
39	LG:228319.2:2002JAN18	411	433		TM	Transmembrane
39	LG:228319.2:2002JAN18	434	585		TM	Extracellular
39	LG:228319.2:2002JAN18	90	152	forward 3	SP	
39	LG:228319.2:2002JAN18	90	143	forward 3	SP	

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
39	LG:228319.2:2002JAN18	90	149	forward 3	SP	
39	LG:228319.2:2002JAN18	90	158	forward 3	SP	
39	LG:228319.2:2002JAN18	39	125	forward 3	SP	
40	LG:229165.16:2002JAN18	1	1023		TM	Extracellular
40	LG:229165.16:2002JAN18	1024	1046		TM	Transmembrane
40	LG:229165.16:2002JAN18	1047	1271		TM	Cytosolic
40	LG:229165.16:2002JAN18	1272	1294		TM	Transmembrane
40	LG:229165.16:2002JAN18	1295	1535		TM	Extracellular
40	LG:229165.16:2002JAN18	1536	1558		TM	Transmembrane
40	LG:229165.16:2002JAN18	1559	1569		TM	Cytosolic
40	LG:229165.16:2002JAN18	1570	1587		TM	Transmembrane
40	LG:229165.16:2002JAN18	1588	1616		TM	Extracellular
40	LG:229165.16:2002JAN18	1	806		TM	Extracellular
40	LG:229165.16:2002JAN18	807	826		TM	Transmembrane
40	LG:229165.16:2002JAN18	827	838		TM	Cytosolic
40	LG:229165.16:2002JAN18	839	861		TM	Transmembrane
40	LG:229165.16:2002JAN18	862	1525		TM	Extracellular
40	LG:229165.16:2002JAN18	1526	1545		TM	Transmembrane
40	LG:229165.16:2002JAN18	1546	1564		TM	Cytosolic
40	LG:229165.16:2002JAN18	1565	1587		TM	Transmembrane
40	LG:229165.16:2002JAN18	1588	1616		TM	Extracellular
40	LG:229165.16:2002JAN18	1	735		TM	Extracellular
40	LG:229165.16:2002JAN18	736	755		TM	Transmembrane
40	LG:229165.16:2002JAN18	756	775		TM	Cytosolic
40	LG:229165.16:2002JAN18	776	798		TM	Transmembrane
40	LG:229165.16:2002JAN18	799	828		TM	Extracellular
40	LG:229165.16:2002JAN18	829	851		TM	Transmembrane
40	LG:229165.16:2002JAN18	852	862		TM	Cytosolic
40	LG:229165.16:2002JAN18	863	885		TM	Transmembrane
40	LG:229165.16:2002JAN18	886	899		TM	Extracellular
40	LG:229165.16:2002JAN18	900	931		TM	Transmembrane
40	LG:229165.16:2002JAN18	932	1270		TM	Cytosolic
40	LG:229165.16:2002JAN18	1271	1293		TM	Transmembrane
40	LG:229165.16:2002JAN18	1294	1302		TM	Extracellular
40	LG:229165.16:2002JAN18	1303	1320		TM	Transmembrane
40	LG:229165.16:2002JAN18	1321	1507		TM	Cytosolic
40	LG:229165.16:2002JAN18	1508	1530		TM	Transmembrane
40	LG:229165.16:2002JAN18	1531	1563		TM	Extracellular
40	LG:229165.16:2002JAN18	1564	1586		TM	Transmembrane
40	LG:229165.16:2002JAN18	1587	1615		TM	Cytosolic
40	LG:229165.16:2002JAN18	2080	2166	forward 1	SP	
40	LG:229165.16:2002JAN18	4676	4753	forward 2	SP	
40	LG:229165.16:2002JAN18	4676	4747	forward 2	SP	
40	LG:229165.16:2002JAN18	4676	4753	forward 2	SP	
40	LG:229165.16:2002JAN18	4698	4772	forward 3	SP	
40	LG:229165.16:2002JAN18	4698	4754	forward 3	SP	
40	LG:229165.16:2002JAN18	4698	4757	forward 3	SP	
40	LG:229165.16:2002JAN18	4698	4778	forward 3	SP	
40	LG:229165.16:2002JAN18	4698	4778	forward 3	SP	

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
40	LG:229165.16:2002JAN18	1404	1496	forward 3	SP	
41	LG:230895.9:2002JAN18	1	138		TM	Cytosolic
41	LG:230895.9:2002JAN18	139	161		TM	Transmembrane
41	LG:230895.9:2002JAN18	162	596		TM	Extracellular
41	LG:230895.9:2002JAN18	749	820	forward 2	SP	
41	LG:230895.9:2002JAN18	749	826	forward 2	SP	
41	LG:230895.9:2002JAN18	749	820	forward 2	SP	
41	LG:230895.9:2002JAN18	749	814	forward 2	SP	
41	LG:230895.9:2002JAN18	749	826	forward 2	SP	
42	LG:233552.5:2002JAN18	1	1187		TM	Extracellular
42	LG:233552.5:2002JAN18	1188	1210		TM	Transmembrane
42	LG:233552.5:2002JAN18	1211	1228		TM	Cytosolic
42	LG:233552.5:2002JAN18	1	793		TM	Extracellular
42	LG:233552.5:2002JAN18	794	816		TM	Transmembrane
42	LG:233552.5:2002JAN18	817	1132		TM	Cytosolic
42	LG:233552.5:2002JAN18	1133	1152		TM	Transmembrane
42	LG:233552.5:2002JAN18	1153	1161		TM	Extracellular
42	LG:233552.5:2002JAN18	1162	1184		TM	Transmembrane
42	LG:233552.5:2002JAN18	1185	1204		TM	Cytosolic
42	LG:233552.5:2002JAN18	1205	1227		TM	Transmembrane
42	LG:233552.5:2002JAN18	1228	1228		TM	Extracellular
42	LG:233552.5:2002JAN18	3379	3432	forward 1	SP	
42	LG:233552.5:2002JAN18	3601	3645	forward 1	SP	
42	LG:233552.5:2002JAN18	719	802	forward 2	SP	
42	LG:233552.5:2002JAN18	746	808	forward 2	SP	
42	LG:233552.5:2002JAN18	746	814	forward 2	SP	
42	LG:233552.5:2002JAN18	719	820	forward 2	SP	
42	LG:233552.5:2002JAN18	170	223	forward 2	SP	
42	LG:233552.5:2002JAN18	170	229	forward 2	SP	
43	LG:234430.7:2002JAN18	2233	2298	forward 1	SP	
43	LG:234430.7:2002JAN18	2233	2292	forward 1	SP	
43	LG:234430.7:2002JAN18	2233	2346	forward 1	SP	
43	LG:234430.7:2002JAN18	1817	1894	forward 2	SP	
43	LG:234430.7:2002JAN18	1817	1894	forward 2	SP	
43	LG:234430.7:2002JAN18	1874	1945	forward 2	SP	
44	LG:236659.1:2002JAN18	1	155		TM	Cytosolic
44	LG:236659.1:2002JAN18	156	178		TM	Transmembrane
44	LG:236659.1:2002JAN18	179	1635		TM	Extracellular
44	LG:236659.1:2002JAN18	1636	1658		TM	Transmembrane
44	LG:236659.1:2002JAN18	1659	1678		TM	Cytosolic
44	LG:236659.1:2002JAN18	1679	1701		TM	Transmembrane
44	LG:236659.1:2002JAN18	1702	1715		TM	Extracellular
44	LG:236659.1:2002JAN18	1716	1734		TM	Transmembrane
44	LG:236659.1:2002JAN18	1735	1740		TM	Cytosolic
44	LG:236659.1:2002JAN18	1741	1760		TM	Transmembrane
44	LG:236659.1:2002JAN18	1761	1794		TM	Extracellular
44	LG:236659.1:2002JAN18	1795	1817		TM	Transmembrane
44	LG:236659.1:2002JAN18	1818	1873		TM	Cytosolic
44	LG:236659.1:2002JAN18	1874	1893		TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
44	LG:236659.1:2002JAN18	1894	2001		TM	Extracellular
44	LG:236659.1:2002JAN18	2002	2024		TM	Transmembrane
44	LG:236659.1:2002JAN18	2025	2093		TM	Cytosolic
44	LG:236659.1:2002JAN18	2094	2116		TM	Transmembrane
44	LG:236659.1:2002JAN18	2117	2334		TM	Extracellular
44	LG:236659.1:2002JAN18	2335	2357		TM	Transmembrane
44	LG:236659.1:2002JAN18	2358	2377		TM	Cytosolic
44	LG:236659.1:2002JAN18	2378	2395		TM	Transmembrane
44	LG:236659.1:2002JAN18	2396	2440		TM	Extracellular
44	LG:236659.1:2002JAN18	2441	2459		TM	Transmembrane
44	LG:236659.1:2002JAN18	2460	2495		TM	Cytosolic
44	LG:236659.1:2002JAN18	2496	2518		TM	Transmembrane
44	LG:236659.1:2002JAN18	2519	2915		TM	Extracellular
44	LG:236659.1:2002JAN18	1	1676		TM	Extracellular
44	LG:236659.1:2002JAN18	1677	1696		TM	Transmembrane
44	LG:236659.1:2002JAN18	1697	1708		TM	Cytosolic
44	LG:236659.1:2002JAN18	1709	1731		TM	Transmembrane
44	LG:236659.1:2002JAN18	1732	1740		TM	Extracellular
44	LG:236659.1:2002JAN18	1741	1760		TM	Transmembrane
44	LG:236659.1:2002JAN18	1761	1780		TM	Cytosolic
44	LG:236659.1:2002JAN18	1781	1803		TM	Transmembrane
44	LG:236659.1:2002JAN18	1804	2473		TM	Extracellular
44	LG:236659.1:2002JAN18	2474	2496		TM	Transmembrane
44	LG:236659.1:2002JAN18	2497	2502		TM	Cytosolic
44	LG:236659.1:2002JAN18	2503	2525		TM	Transmembrane
44	LG:236659.1:2002JAN18	2526	2914		TM	Extracellular
44	LG:236659.1:2002JAN18	1	1736		TM	Extracellular
44	LG:236659.1:2002JAN18	1737	1759		TM	Transmembrane
44	LG:236659.1:2002JAN18	1760	1993		TM	Cytosolic
44	LG:236659.1:2002JAN18	1994	2016		TM	Transmembrane
44	LG:236659.1:2002JAN18	2017	2020		TM	Extracellular
44	LG:236659.1:2002JAN18	2021	2038		TM	Transmembrane
44	LG:236659.1:2002JAN18	2039	2335		TM	Cytosolic
44	LG:236659.1:2002JAN18	2336	2358		TM	Transmembrane
44	LG:236659.1:2002JAN18	2359	2914		TM	Extracellular
44	LG:236659.1:2002JAN18	5200	5262	forward 1	SP	
44	LG:236659.1:2002JAN18	3833	3895	forward 2	SP	
44	LG:236659.1:2002JAN18	6732	6797	forward 3	SP	
44	LG:236659.1:2002JAN18	1026	1106	forward 3	SP	
44	LG:236659.1:2002JAN18	1026	1100	forward 3	SP	
45	LG:236767.26:2002JAN18	1118	1189	forward 2	SP	
45	LG:236767.26:2002JAN18	1118	1195	forward 2	SP	
45	LG:236767.26:2002JAN18	1118	1189	forward 2	SP	
45	LG:236767.26:2002JAN18	1118	1183	forward 2	SP	
46	LG:237489.7:2002JAN18	1	70		TM	Extracellular
46	LG:237489.7:2002JAN18	71	93		TM	Transmembrane
46	LG:237489.7:2002JAN18	94	94		TM	Cytosolic
46	LG:237489.7:2002JAN18	95	117		TM	Transmembrane
46	LG:237489.7:2002JAN18	118	1144		TM	Extracellular

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
46	LG:237489.7:2002JAN18	1	1123		TM	Extracellular
46	LG:237489.7:2002JAN18	1124	1143		TM	Transmembrane
46	LG:237489.7:2002JAN18	1144	1144		TM	Cytosolic
46	LG:237489.7:2002JAN18	1	1113		TM	Extracellular
46	LG:237489.7:2002JAN18	1114	1136		TM	Transmembrane
46	LG:237489.7:2002JAN18	1137	1143		TM	Cytosolic
46	LG:237489.7:2002JAN18	1096	1152	forward 1	SP	
46	LG:237489.7:2002JAN18	1568	1684	forward 2	SP	
46	LG:237489.7:2002JAN18	2484	2564	forward 3	SP	
46	LG:237489.7:2002JAN18	2484	2558	forward 3	SP	
46	LG:237489.7:2002JAN18	2484	2567	forward 3	SP	
46	LG:237489.7:2002JAN18	2484	2555	forward 3	SP	
46	LG:237489.7:2002JAN18	2484	2573	forward 3	SP	
46	LG:237489.7:2002JAN18	2484	2549	forward 3	SP	
46	LG:237489.7:2002JAN18	2484	2564	forward 3	SP	
47	LG:238218.20:2002JAN18	1	794		TM	Extracellular
47	LG:238218.20:2002JAN18	795	817		TM	Transmembrane
47	LG:238218.20:2002JAN18	818	1053		TM	Cytosolic
47	LG:238218.20:2002JAN18	1054	1076		TM	Transmembrane
47	LG:238218.20:2002JAN18	1077	1090		TM	Extracellular
47	LG:238218.20:2002JAN18	1091	1113		TM	Transmembrane
47	LG:238218.20:2002JAN18	1114	1265		TM	Cytosolic
47	LG:238218.20:2002JAN18	1266	1288		TM	Transmembrane
47	LG:238218.20:2002JAN18	1289	1630		TM	Extracellular
47	LG:238218.20:2002JAN18	1631	1653		TM	Transmembrane
47	LG:238218.20:2002JAN18	1654	1735		TM	Cytosolic
47	LG:238218.20:2002JAN18	1736	1758		TM	Transmembrane
47	LG:238218.20:2002JAN18	1759	1761		TM	Extracellular
47	LG:238218.20:2002JAN18	1762	1779		TM	Transmembrane
47	LG:238218.20:2002JAN18	1780	1799		TM	Cytosolic
47	LG:238218.20:2002JAN18	1800	1822		TM	Transmembrane
47	LG:238218.20:2002JAN18	1823	1836		TM	Extracellular
47	LG:238218.20:2002JAN18	1837	1859		TM	Transmembrane
47	LG:238218.20:2002JAN18	1860	2005		TM	Cytosolic
47	LG:238218.20:2002JAN18	1	1584		TM	Extracellular
47	LG:238218.20:2002JAN18	1585	1607		TM	Transmembrane
47	LG:238218.20:2002JAN18	1608	1639		TM	Cytosolic
47	LG:238218.20:2002JAN18	1640	1662		TM	Transmembrane
47	LG:238218.20:2002JAN18	1663	2005		TM	Extracellular
47	LG:238218.20:2002JAN18	1	1090		TM	Extracellular
47	LG:238218.20:2002JAN18	1091	1113		TM	Transmembrane
47	LG:238218.20:2002JAN18	1114	1142		TM	Cytosolic
47	LG:238218.20:2002JAN18	1143	1165		TM	Transmembrane
47	LG:238218.20:2002JAN18	1166	1222		TM	Extracellular
47	LG:238218.20:2002JAN18	1223	1245		TM	Transmembrane
47	LG:238218.20:2002JAN18	1246	1265		TM	Cytosolic
47	LG:238218.20:2002JAN18	1266	1288		TM	Transmembrane
47	LG:238218.20:2002JAN18	1289	1793		TM	Extracellular
47	LG:238218.20:2002JAN18	1794	1816		TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
47	LG:238218.20:2002JAN18	1817	1836		TM	Cytosolic
47	LG:238218.20:2002JAN18	1837	1859		TM	Transmembrane
47	LG:238218.20:2002JAN18	1860	2005		TM	Extracellular
47	LG:238218.20:2002JAN18	3814	3900	forward 1	SP	
47	LG:238218.20:2002JAN18	3814	3879	forward 1	SP	
47	LG:238218.20:2002JAN18	3814	3891	forward 1	SP	
47	LG:238218.20:2002JAN18	4927	4980	forward 1	SP	
47	LG:238218.20:2002JAN18	3814	3891	forward 1	SP	
47	LG:238218.20:2002JAN18	4927	4974	forward 1	SP	
47	LG:238218.20:2002JAN18	3814	3885	forward 1	SP	
47	LG:238218.20:2002JAN18	4927	4989	forward 1	SP	
47	LG:238218.20:2002JAN18	4900	4992	forward 1	SP	
47	LG:238218.20:2002JAN18	4927	4980	forward 1	SP	
47	LG:238218.20:2002JAN18	3814	3885	forward 1	SP	
47	LG:238218.20:2002JAN18	518	598	forward 2	SP	
47	LG:238218.20:2002JAN18	518	598	forward 2	SP	
47	LG:238218.20:2002JAN18	518	583	forward 2	SP	
47	LG:238218.20:2002JAN18	518	586	forward 2	SP	
47	LG:238218.20:2002JAN18	518	601	forward 2	SP	
47	LG:238218.20:2002JAN18	518	565	forward 2	SP	
47	LG:238218.20:2002JAN18	518	571	forward 2	SP	
47	LG:238218.20:2002JAN18	2400	2456	forward 3	SP	
47	LG:238218.20:2002JAN18	2400	2459	forward 3	SP	
47	LG:238218.20:2002JAN18	1941	2009	forward 3	SP	
47	LG:238218.20:2002JAN18	1941	2015	forward 3	SP	
47	LG:238218.20:2002JAN18	1941	2003	forward 3	SP	
47	LG:238218.20:2002JAN18	1941	2015	forward 3	SP	
47	LG:238218.20:2002JAN18	1941	2015	forward 3	SP	
48	LG:239939.14:2002JAN18	1	3		TM	Extracellular
48	LG:239939.14:2002JAN18	4	26		TM	Transmembrane
48	LG:239939.14:2002JAN18	27	149		TM	Cytosolic
48	LG:239939.14:2002JAN18	150	169		TM	Transmembrane
48	LG:239939.14:2002JAN18	170	183		TM	Extracellular
48	LG:239939.14:2002JAN18	184	206		TM	Transmembrane
48	LG:239939.14:2002JAN18	207	379		TM	Cytosolic
48	LG:239939.14:2002JAN18	380	402		TM	Transmembrane
48	LG:239939.14:2002JAN18	403	434		TM	Extracellular
48	LG:239939.14:2002JAN18	873	926	forward 3	SP	
48	LG:239939.14:2002JAN18	873	929	forward 3	SP	
48	LG:239939.14:2002JAN18	873	956	forward 3	SP	
49	LG:242288.11:2002JAN18	973	1044	forward 1	SP	
49	LG:242288.11:2002JAN18	4097	4195	forward 2	SP	
50	LG:242491.29:2002JAN18	64	117	forward 1	SP	
50	LG:242491.29:2002JAN18	64	120	forward 1	SP	
50	LG:242491.29:2002JAN18	64	123	forward 1	SP	
50	LG:242491.29:2002JAN18	31	117	forward 1	SP	
50	LG:242491.29:2002JAN18	64	126	forward 1	SP	
50	LG:242491.29:2002JAN18	64	117	forward 1	SP	
50	LG:242491.29:2002JAN18	31	123	forward 1	SP	

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
50	LG:242491.29:2002JAN18	64	129	forward 1	SP	
50	LG:242491.29:2002JAN18	43	117	forward 1	SP	
50	LG:242491.29:2002JAN18	31	123	forward 1	SP	
51	LG:243488.41:2002JAN18	1	525		TM	Extracellular
51	LG:243488.41:2002JAN18	526	548		TM	Transmembrane
51	LG:243488.41:2002JAN18	549	655		TM	Cytosolic
51	LG:243488.41:2002JAN18	656	678		TM	Transmembrane
51	LG:243488.41:2002JAN18	679	715		TM	Extracellular
51	LG:243488.41:2002JAN18	716	735		TM	Transmembrane
51	LG:243488.41:2002JAN18	736	742		TM	Cytosolic
51	LG:243488.41:2002JAN18	1	665		TM	Extracellular
51	LG:243488.41:2002JAN18	666	688		TM	Transmembrane
51	LG:243488.41:2002JAN18	689	742		TM	Cytosolic
51	LG:243488.41:2002JAN18	361	438	forward 1	SP	
51	LG:243488.41:2002JAN18	1940	2017	forward 2	SP	
51	LG:243488.41:2002JAN18	1940	2020	forward 2	SP	
52	LG:247792.18:2002JAN18	1	1050		TM	Extracellular
52	LG:247792.18:2002JAN18	1051	1073		TM	Transmembrane
52	LG:247792.18:2002JAN18	1074	1142		TM	Cytosolic
52	LG:247792.18:2002JAN18	1930	2016	forward 1	SP	
52	LG:247792.18:2002JAN18	1930	2010	forward 1	SP	
53	LG:253193.17:2002JAN18	1	201		TM	Extracellular
53	LG:253193.17:2002JAN18	202	224		TM	Transmembrane
53	LG:253193.17:2002JAN18	225	440		TM	Cytosolic
53	LG:253193.17:2002JAN18	441	463		TM	Transmembrane
53	LG:253193.17:2002JAN18	464	771		TM	Extracellular
53	LG:253193.17:2002JAN18	1	52		TM	Cytosolic
53	LG:253193.17:2002JAN18	53	75		TM	Transmembrane
53	LG:253193.17:2002JAN18	76	84		TM	Extracellular
53	LG:253193.17:2002JAN18	85	107		TM	Transmembrane
53	LG:253193.17:2002JAN18	108	200		TM	Cytosolic
53	LG:253193.17:2002JAN18	201	223		TM	Transmembrane
53	LG:253193.17:2002JAN18	224	291		TM	Extracellular
53	LG:253193.17:2002JAN18	292	314		TM	Transmembrane
53	LG:253193.17:2002JAN18	315	371		TM	Cytosolic
53	LG:253193.17:2002JAN18	372	394		TM	Transmembrane
53	LG:253193.17:2002JAN18	395	770		TM	Extracellular
53	LG:253193.17:2002JAN18	1	20		TM	Cytosolic
53	LG:253193.17:2002JAN18	21	40		TM	Transmembrane
53	LG:253193.17:2002JAN18	41	49		TM	Extracellular
53	LG:253193.17:2002JAN18	50	72		TM	Transmembrane
53	LG:253193.17:2002JAN18	73	152		TM	Cytosolic
53	LG:253193.17:2002JAN18	153	171		TM	Transmembrane
53	LG:253193.17:2002JAN18	172	211		TM	Extracellular
53	LG:253193.17:2002JAN18	212	234		TM	Transmembrane
53	LG:253193.17:2002JAN18	235	290		TM	Cytosolic
53	LG:253193.17:2002JAN18	291	313		TM	Transmembrane
53	LG:253193.17:2002JAN18	314	770		TM	Extracellular
53	LG:253193.17:2002JAN18	1513	1578	forward 1	SP	

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
53	LG:253193.17:2002JAN18	257	322	forward 2	SP	
53	LG:253193.17:2002JAN18	257	319	forward 2	SP	
54	LG:257088.20:2002JAN18	1	20		TM	Cytosolic
54	LG:257088.20:2002JAN18	21	43		TM	Transmembrane
54	LG:257088.20:2002JAN18	44	1253		TM	Extracellular
54	LG:257088.20:2002JAN18	1028	1153	forward 2	SP	
54	LG:257088.20:2002JAN18	1028	1147	forward 2	SP	
54	LG:257088.20:2002JAN18	1937	1999	forward 2	SP	
55	LG:265552.1:2002JAN18	1	218		TM	Cytosolic
55	LG:265552.1:2002JAN18	219	238		TM	Transmembrane
55	LG:265552.1:2002JAN18	239	247		TM	Extracellular
55	LG:265552.1:2002JAN18	248	267		TM	Transmembrane
55	LG:265552.1:2002JAN18	268	341		TM	Cytosolic
55	LG:265552.1:2002JAN18	342	364		TM	Transmembrane
55	LG:265552.1:2002JAN18	365	630		TM	Extracellular
55	LG:265552.1:2002JAN18	1	163		TM	Extracellular
55	LG:265552.1:2002JAN18	164	186		TM	Transmembrane
55	LG:265552.1:2002JAN18	187	226		TM	Cytosolic
55	LG:265552.1:2002JAN18	227	249		TM	Transmembrane
55	LG:265552.1:2002JAN18	250	291		TM	Extracellular
55	LG:265552.1:2002JAN18	292	314		TM	Transmembrane
55	LG:265552.1:2002JAN18	315	629		TM	Cytosolic
55	LG:265552.1:2002JAN18	1	381		TM	Extracellular
55	LG:265552.1:2002JAN18	382	404		TM	Transmembrane
55	LG:265552.1:2002JAN18	405	483		TM	Cytosolic
55	LG:265552.1:2002JAN18	484	506		TM	Transmembrane
55	LG:265552.1:2002JAN18	507	629		TM	Extracellular
55	LG:265552.1:2002JAN18	817	867	forward 1	SP	
55	LG:265552.1:2002JAN18	683	754	forward 2	SP	
55	LG:265552.1:2002JAN18	683	742	forward 2	SP	
55	LG:265552.1:2002JAN18	683	760	forward 2	SP	
55	LG:265552.1:2002JAN18	683	748	forward 2	SP	
55	LG:265552.1:2002JAN18	683	757	forward 2	SP	
55	LG:265552.1:2002JAN18	683	745	forward 2	SP	
55	LG:265552.1:2002JAN18	683	748	forward 2	SP	
56	LG:275355.12:2002JAN18	1	386		TM	Extracellular
56	LG:275355.12:2002JAN18	387	409		TM	Transmembrane
56	LG:275355.12:2002JAN18	410	429		TM	Cytosolic
56	LG:275355.12:2002JAN18	430	452		TM	Transmembrane
56	LG:275355.12:2002JAN18	453	514		TM	Extracellular
56	LG:275355.12:2002JAN18	1	387		TM	Extracellular
56	LG:275355.12:2002JAN18	388	410		TM	Transmembrane
56	LG:275355.12:2002JAN18	411	429		TM	Cytosolic
56	LG:275355.12:2002JAN18	430	452		TM	Transmembrane
56	LG:275355.12:2002JAN18	453	513		TM	Extracellular
56	LG:275355.12:2002JAN18	1084	1155	forward 1	SP	
56	LG:275355.12:2002JAN18	1084	1161	forward 1	SP	
56	LG:275355.12:2002JAN18	1084	1161	forward 1	SP	
56	LG:275355.12:2002JAN18	86	145	forward 2	SP	

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
57	LG:280014.1:2002JAN18	1	100		TM	Extracellular
57	LG:280014.1:2002JAN18	101	123		TM	Transmembrane
57	LG:280014.1:2002JAN18	124	238		TM	Cytosolic
57	LG:280014.1:2002JAN18	239	256		TM	Transmembrane
57	LG:280014.1:2002JAN18	257	270		TM	Extracellular
57	LG:280014.1:2002JAN18	271	293		TM	Transmembrane
57	LG:280014.1:2002JAN18	294	314		TM	Cytosolic
57	LG:280014.1:2002JAN18	315	334		TM	Transmembrane
57	LG:280014.1:2002JAN18	335	335		TM	Extracellular
57	LG:280014.1:2002JAN18	1	99		TM	Extracellular
57	LG:280014.1:2002JAN18	100	122		TM	Transmembrane
57	LG:280014.1:2002JAN18	123	335		TM	Cytosolic
57	LG:280014.1:2002JAN18	457	543	forward 1	SP	
57	LG:280014.1:2002JAN18	457	537	forward 1	SP	
57	LG:280014.1:2002JAN18	457	528	forward 1	SP	
57	LG:280014.1:2002JAN18	457	528	forward 1	SP	
57	LG:280014.1:2002JAN18	457	543	forward 1	SP	
57	LG:280014.1:2002JAN18	712	765	forward 1	SP	
57	LG:280014.1:2002JAN18	457	549	forward 1	SP	
57	LG:280014.1:2002JAN18	165	239	forward 3	SP	
57	LG:280014.1:2002JAN18	165	236	forward 3	SP	
57	LG:280014.1:2002JAN18	165	236	forward 3	SP	
57	LG:280014.1:2002JAN18	165	251	forward 3	SP	
57	LG:280014.1:2002JAN18	165	242	forward 3	SP	
57	LG:280014.1:2002JAN18	267	335	forward 3	SP	
58	LG:299937.3:2002JAN18	1	790		TM	Extracellular
58	LG:299937.3:2002JAN18	791	813		TM	Transmembrane
58	LG:299937.3:2002JAN18	814	1010		TM	Cytosolic
58	LG:299937.3:2002JAN18	817	888	forward 1	SP	
58	LG:299937.3:2002JAN18	2726	2785	forward 2	SP	
59	LG:311197.3:2002JAN18	1	1547		TM	Extracellular
59	LG:311197.3:2002JAN18	1548	1570		TM	Transmembrane
59	LG:311197.3:2002JAN18	1571	1584		TM	Cytosolic
59	LG:311197.3:2002JAN18	2227	2307	forward 1	SP	
59	LG:311197.3:2002JAN18	2227	2322	forward 1	SP	
59	LG:311197.3:2002JAN18	4552	4608	forward 1	SP	
59	LG:311197.3:2002JAN18	4552	4614	forward 1	SP	
59	LG:311197.3:2002JAN18	2850	2915	forward 3	SP	
59	LG:311197.3:2002JAN18	2850	2921	forward 3	SP	
59	LG:311197.3:2002JAN18	675	761	forward 3	SP	
60	LG:321069.2:2002JAN18	1	630		TM	Extracellular
60	LG:321069.2:2002JAN18	631	653		TM	Transmembrane
60	LG:321069.2:2002JAN18	654	665		TM	Cytosolic
60	LG:321069.2:2002JAN18	666	688		TM	Transmembrane
60	LG:321069.2:2002JAN18	689	702		TM	Extracellular
60	LG:321069.2:2002JAN18	703	725		TM	Transmembrane
60	LG:321069.2:2002JAN18	726	886		TM	Cytosolic
60	LG:321069.2:2002JAN18	887	909		TM	Transmembrane
60	LG:321069.2:2002JAN18	910	1343		TM	Extracellular

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
60	LG:321069.2:2002JAN18	1	634		TM	Extracellular
60	LG:321069.2:2002JAN18	635	653		TM	Transmembrane
60	LG:321069.2:2002JAN18	654	664		TM	Cytosolic
60	LG:321069.2:2002JAN18	665	687		TM	Transmembrane
60	LG:321069.2:2002JAN18	688	806		TM	Extracellular
60	LG:321069.2:2002JAN18	807	829		TM	Transmembrane
60	LG:321069.2:2002JAN18	830	1078		TM	Cytosolic
60	LG:321069.2:2002JAN18	1079	1101		TM	Transmembrane
60	LG:321069.2:2002JAN18	1102	1127		TM	Extracellular
60	LG:321069.2:2002JAN18	1128	1150		TM	Transmembrane
60	LG:321069.2:2002JAN18	1151	1343		TM	Cytosolic
60	LG:321069.2:2002JAN18	1	448		TM	Cytosolic
60	LG:321069.2:2002JAN18	449	468		TM	Transmembrane
60	LG:321069.2:2002JAN18	469	477		TM	Extracellular
60	LG:321069.2:2002JAN18	478	500		TM	Transmembrane
60	LG:321069.2:2002JAN18	501	506		TM	Cytosolic
60	LG:321069.2:2002JAN18	507	529		TM	Transmembrane
60	LG:321069.2:2002JAN18	530	630		TM	Extracellular
60	LG:321069.2:2002JAN18	631	653		TM	Transmembrane
60	LG:321069.2:2002JAN18	654	665		TM	Cytosolic
60	LG:321069.2:2002JAN18	666	688		TM	Transmembrane
60	LG:321069.2:2002JAN18	689	692		TM	Extracellular
60	LG:321069.2:2002JAN18	693	712		TM	Transmembrane
60	LG:321069.2:2002JAN18	713	1070		TM	Cytosolic
60	LG:321069.2:2002JAN18	1071	1093		TM	Transmembrane
60	LG:321069.2:2002JAN18	1094	1102		TM	Extracellular
60	LG:321069.2:2002JAN18	1103	1122		TM	Transmembrane
60	LG:321069.2:2002JAN18	1123	1128		TM	Cytosolic
60	LG:321069.2:2002JAN18	1129	1151		TM	Transmembrane
60	LG:321069.2:2002JAN18	1152	1343		TM	Extracellular
60	LG:321069.2:2002JAN18	535	600	forward 1	SP	
60	LG:321069.2:2002JAN18	535	606	forward 1	SP	
61	LG:330900.8:2002JAN18	1	1252		TM	Extracellular
61	LG:330900.8:2002JAN18	1253	1275		TM	Transmembrane
61	LG:330900.8:2002JAN18	1276	1294		TM	Cytosolic
61	LG:330900.8:2002JAN18	1295	1317		TM	Transmembrane
61	LG:330900.8:2002JAN18	1318	1326		TM	Extracellular
61	LG:330900.8:2002JAN18	1327	1349		TM	Transmembrane
61	LG:330900.8:2002JAN18	1350	1360		TM	Cytosolic
61	LG:330900.8:2002JAN18	1361	1383		TM	Transmembrane
61	LG:330900.8:2002JAN18	1384	1458		TM	Extracellular
61	LG:330900.8:2002JAN18	1459	1481		TM	Transmembrane
61	LG:330900.8:2002JAN18	1482	1501		TM	Cytosolic
61	LG:330900.8:2002JAN18	1502	1524		TM	Transmembrane
61	LG:330900.8:2002JAN18	1525	1577		TM	Extracellular
61	LG:330900.8:2002JAN18	1578	1600		TM	Transmembrane
61	LG:330900.8:2002JAN18	1601	1630		TM	Cytosolic
61	LG:330900.8:2002JAN18	1631	1653		TM	Transmembrane
61	LG:330900.8:2002JAN18	1654	1678		TM	Extracellular

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
61	LG:330900.8:2002JAN18	1	1649		TM	Extracellular
61	LG:330900.8:2002JAN18	1650	1672		TM	Transmembrane
61	LG:330900.8:2002JAN18	1673	1678		TM	Cytosolic
61	LG:330900.8:2002JAN18	1	22		TM	Extracellular
61	LG:330900.8:2002JAN18	23	45		TM	Transmembrane
61	LG:330900.8:2002JAN18	46	115		TM	Cytosolic
61	LG:330900.8:2002JAN18	116	135		TM	Transmembrane
61	LG:330900.8:2002JAN18	136	437		TM	Extracellular
61	LG:330900.8:2002JAN18	438	460		TM	Transmembrane
61	LG:330900.8:2002JAN18	461	596		TM	Cytosolic
61	LG:330900.8:2002JAN18	597	619		TM	Transmembrane
61	LG:330900.8:2002JAN18	620	633		TM	Extracellular
61	LG:330900.8:2002JAN18	634	651		TM	Transmembrane
61	LG:330900.8:2002JAN18	652	671		TM	Cytosolic
61	LG:330900.8:2002JAN18	672	694		TM	Transmembrane
61	LG:330900.8:2002JAN18	695	1356		TM	Extracellular
61	LG:330900.8:2002JAN18	1357	1376		TM	Transmembrane
61	LG:330900.8:2002JAN18	1377	1380		TM	Cytosolic
61	LG:330900.8:2002JAN18	1381	1403		TM	Transmembrane
61	LG:330900.8:2002JAN18	1404	1433		TM	Extracellular
61	LG:330900.8:2002JAN18	1434	1456		TM	Transmembrane
61	LG:330900.8:2002JAN18	1457	1476		TM	Cytosolic
61	LG:330900.8:2002JAN18	1477	1499		TM	Transmembrane
61	LG:330900.8:2002JAN18	1500	1503		TM	Extracellular
61	LG:330900.8:2002JAN18	1504	1526		TM	Transmembrane
61	LG:330900.8:2002JAN18	1527	1654		TM	Cytosolic
61	LG:330900.8:2002JAN18	1655	1672		TM	Transmembrane
61	LG:330900.8:2002JAN18	1673	1677		TM	Extracellular
61	LG:330900.8:2002JAN18	3012	3089	forward 3	SP	
61	LG:330900.8:2002JAN18	3012	3083	forward 3	SP	
61	LG:330900.8:2002JAN18	3012	3089	forward 3	SP	
61	LG:330900.8:2002JAN18	3012	3074	forward 3	SP	
61	LG:330900.8:2002JAN18	3012	3083	forward 3	SP	
61	LG:330900.8:2002JAN18	3012	3077	forward 3	SP	
61	LG:330900.8:2002JAN18	3012	3089	forward 3	SP	
61	LG:330900.8:2002JAN18	3012	3095	forward 3	SP	
61	LG:330900.8:2002JAN18	3012	3080	forward 3	SP	
61	LG:330900.8:2002JAN18	3012	3095	forward 3	SP	
61	LG:330900.8:2002JAN18	3027	3083	forward 3	SP	
62	LG:330931.9:2002JAN18	1	1400		TM	Extracellular
62	LG:330931.9:2002JAN18	1401	1423		TM	Transmembrane
62	LG:330931.9:2002JAN18	1424	1429		TM	Cytosolic
62	LG:330931.9:2002JAN18	1430	1447		TM	Transmembrane
62	LG:330931.9:2002JAN18	1448	1701		TM	Extracellular
62	LG:330931.9:2002JAN18	1702	1724		TM	Transmembrane
62	LG:330931.9:2002JAN18	1725	1816		TM	Cytosolic
62	LG:330931.9:2002JAN18	1817	1839		TM	Transmembrane
62	LG:330931.9:2002JAN18	1840	1853		TM	Extracellular
62	LG:330931.9:2002JAN18	1854	1873		TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
62	LG:330931.9:2002JAN18	1874	1950		TM	Cytosolic
62	LG:330931.9:2002JAN18	1951	1973		TM	Transmembrane
62	LG:330931.9:2002JAN18	1974	1992		TM	Extracellular
62	LG:330931.9:2002JAN18	1993	2015		TM	Transmembrane
62	LG:330931.9:2002JAN18	2016	2035		TM	Cytosolic
62	LG:330931.9:2002JAN18	1	1109		TM	Extracellular
62	LG:330931.9:2002JAN18	1110	1132		TM	Transmembrane
62	LG:330931.9:2002JAN18	1133	1144		TM	Cytosolic
62	LG:330931.9:2002JAN18	1145	1167		TM	Transmembrane
62	LG:330931.9:2002JAN18	1168	1701		TM	Extracellular
62	LG:330931.9:2002JAN18	1702	1724		TM	Transmembrane
62	LG:330931.9:2002JAN18	1725	1822		TM	Cytosolic
62	LG:330931.9:2002JAN18	1823	1845		TM	Transmembrane
62	LG:330931.9:2002JAN18	1846	1859		TM	Extracellular
62	LG:330931.9:2002JAN18	1860	1875		TM	Transmembrane
62	LG:330931.9:2002JAN18	1876	1939		TM	Cytosolic
62	LG:330931.9:2002JAN18	1940	1962		TM	Transmembrane
62	LG:330931.9:2002JAN18	1963	1996		TM	Extracellular
62	LG:330931.9:2002JAN18	1997	2019		TM	Transmembrane
62	LG:330931.9:2002JAN18	2020	2035		TM	Cytosolic
62	LG:330931.9:2002JAN18	2662	2721	forward 1	SP	
62	LG:330931.9:2002JAN18	2662	2727	forward 1	SP	
62	LG:330931.9:2002JAN18	4906	4971	forward 1	SP	
62	LG:330931.9:2002JAN18	4906	4962	forward 1	SP	
62	LG:330931.9:2002JAN18	1826	1888	forward 2	SP	
62	LG:330931.9:2002JAN18	2073	2180	forward 3	SP	
63	LG:330985.1:2002JAN18	1	106		TM	Cytosolic
63	LG:330985.1:2002JAN18	107	129		TM	Transmembrane
63	LG:330985.1:2002JAN18	130	133		TM	Extracellular
63	LG:330985.1:2002JAN18	134	156		TM	Transmembrane
63	LG:330985.1:2002JAN18	157	162		TM	Cytosolic
63	LG:330985.1:2002JAN18	163	182		TM	Transmembrane
63	LG:330985.1:2002JAN18	183	196		TM	Extracellular
63	LG:330985.1:2002JAN18	197	216		TM	Transmembrane
63	LG:330985.1:2002JAN18	217	222		TM	Cytosolic
63	LG:330985.1:2002JAN18	223	242		TM	Transmembrane
63	LG:330985.1:2002JAN18	243	308		TM	Extracellular
63	LG:330985.1:2002JAN18	309	331		TM	Transmembrane
63	LG:330985.1:2002JAN18	332	342		TM	Cytosolic
63	LG:330985.1:2002JAN18	343	365		TM	Transmembrane
63	LG:330985.1:2002JAN18	366	369		TM	Extracellular
63	LG:330985.1:2002JAN18	370	392		TM	Transmembrane
63	LG:330985.1:2002JAN18	393	398		TM	Cytosolic
63	LG:330985.1:2002JAN18	399	421		TM	Transmembrane
63	LG:330985.1:2002JAN18	422	435		TM	Extracellular
63	LG:330985.1:2002JAN18	436	458		TM	Transmembrane
63	LG:330985.1:2002JAN18	459	470		TM	Cytosolic
63	LG:330985.1:2002JAN18	471	490		TM	Transmembrane
63	LG:330985.1:2002JAN18	491	1078		TM	Extracellular

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
63	LG:330985.1:2002JAN18	1798	1857	forward 1	SP	
63	LG:330985.1:2002JAN18	1798	1869	forward 1	SP	
63	LG:330985.1:2002JAN18	1798	1875	forward 1	SP	
63	LG:330985.1:2002JAN18	1798	1872	forward 1	SP	
63	LG:330985.1:2002JAN18	550	639	forward 1	SP	
63	LG:330985.1:2002JAN18	1798	1863	forward 1	SP	
63	LG:330985.1:2002JAN18	1798	1842	forward 1	SP	
63	LG:330985.1:2002JAN18	417	476	forward 3	SP	
64	LG:332027.9:2002JAN18	1	570		TM	Extracellular
64	LG:332027.9:2002JAN18	571	593		TM	Transmembrane
64	LG:332027.9:2002JAN18	594	613		TM	Cytosolic
64	LG:332027.9:2002JAN18	614	636		TM	Transmembrane
64	LG:332027.9:2002JAN18	637	655		TM	Extracellular
64	LG:332027.9:2002JAN18	656	678		TM	Transmembrane
64	LG:332027.9:2002JAN18	679	865		TM	Cytosolic
64	LG:332027.9:2002JAN18	866	888		TM	Transmembrane
64	LG:332027.9:2002JAN18	889	968		TM	Extracellular
64	LG:332027.9:2002JAN18	969	988		TM	Transmembrane
64	LG:332027.9:2002JAN18	989	1022		TM	Cytosolic
64	LG:332027.9:2002JAN18	1	449		TM	Extracellular
64	LG:332027.9:2002JAN18	450	472		TM	Transmembrane
64	LG:332027.9:2002JAN18	473	553		TM	Cytosolic
64	LG:332027.9:2002JAN18	554	576		TM	Transmembrane
64	LG:332027.9:2002JAN18	577	624		TM	Extracellular
64	LG:332027.9:2002JAN18	625	644		TM	Transmembrane
64	LG:332027.9:2002JAN18	645	859		TM	Cytosolic
64	LG:332027.9:2002JAN18	860	882		TM	Transmembrane
64	LG:332027.9:2002JAN18	883	918		TM	Extracellular
64	LG:332027.9:2002JAN18	919	941		TM	Transmembrane
64	LG:332027.9:2002JAN18	942	961		TM	Cytosolic
64	LG:332027.9:2002JAN18	962	984		TM	Transmembrane
64	LG:332027.9:2002JAN18	985	1021		TM	Extracellular
64	LG:332027.9:2002JAN18	1	750		TM	Extracellular
64	LG:332027.9:2002JAN18	751	773		TM	Transmembrane
64	LG:332027.9:2002JAN18	774	800		TM	Cytosolic
64	LG:332027.9:2002JAN18	801	823		TM	Transmembrane
64	LG:332027.9:2002JAN18	824	872		TM	Extracellular
64	LG:332027.9:2002JAN18	873	895		TM	Transmembrane
64	LG:332027.9:2002JAN18	896	948		TM	Cytosolic
64	LG:332027.9:2002JAN18	949	971		TM	Transmembrane
64	LG:332027.9:2002JAN18	972	1021		TM	Extracellular
65	LG:335377.8:2002JAN18	3010	3108	forward 1	SP	
65	LG:335377.8:2002JAN18	3010	3084	forward 1	SP	
65	LG:335377.8:2002JAN18	2090	2143	forward 2	SP	
65	LG:335377.8:2002JAN18	2883	2945	forward 3	SP	
65	LG:335377.8:2002JAN18	2883	2957	forward 3	SP	
65	LG:335377.8:2002JAN18	2883	2951	forward 3	SP	
65	LG:335377.8:2002JAN18	3030	3110	forward 3	SP	
65	LG:335377.8:2002JAN18	2883	2948	forward 3	SP	

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
66	LG:337452.25:2002JAN18	1156	1233	forward 1	SP	
66	LG:337452.25:2002JAN18	2237	2314	forward 2	SP	
66	LG:337452.25:2002JAN18	1514	1600	forward 2	SP	
67	LG:340580.16:2002JAN18	1	393		TM	Extracellular
67	LG:340580.16:2002JAN18	394	416		TM	Transmembrane
67	LG:340580.16:2002JAN18	417	422		TM	Cytosolic
67	LG:340580.16:2002JAN18	423	440		TM	Transmembrane
67	LG:340580.16:2002JAN18	441	1131		TM	Extracellular
67	LG:340580.16:2002JAN18	1132	1151		TM	Transmembrane
67	LG:340580.16:2002JAN18	1152	1685		TM	Cytosolic
67	LG:340580.16:2002JAN18	1686	1708		TM	Transmembrane
67	LG:340580.16:2002JAN18	1709	1722		TM	Extracellular
67	LG:340580.16:2002JAN18	1723	1745		TM	Transmembrane
67	LG:340580.16:2002JAN18	1746	1796		TM	Cytosolic
67	LG:340580.16:2002JAN18	1797	1819		TM	Transmembrane
67	LG:340580.16:2002JAN18	1820	1881		TM	Extracellular
67	LG:340580.16:2002JAN18	1882	1901		TM	Transmembrane
67	LG:340580.16:2002JAN18	1902	1975		TM	Cytosolic
67	LG:340580.16:2002JAN18	1976	1998		TM	Transmembrane
67	LG:340580.16:2002JAN18	1999	2288		TM	Extracellular
67	LG:340580.16:2002JAN18	2289	2311		TM	Transmembrane
67	LG:340580.16:2002JAN18	2312	2317		TM	Cytosolic
67	LG:340580.16:2002JAN18	2318	2335		TM	Transmembrane
67	LG:340580.16:2002JAN18	2336	2446		TM	Extracellular
67	LG:340580.16:2002JAN18	1	42		TM	Cytosolic
67	LG:340580.16:2002JAN18	43	61		TM	Transmembrane
67	LG:340580.16:2002JAN18	62	80		TM	Extracellular
67	LG:340580.16:2002JAN18	81	98		TM	Transmembrane
67	LG:340580.16:2002JAN18	99	197		TM	Cytosolic
67	LG:340580.16:2002JAN18	198	220		TM	Transmembrane
67	LG:340580.16:2002JAN18	221	393		TM	Extracellular
67	LG:340580.16:2002JAN18	394	416		TM	Transmembrane
67	LG:340580.16:2002JAN18	417	428		TM	Cytosolic
67	LG:340580.16:2002JAN18	429	451		TM	Transmembrane
67	LG:340580.16:2002JAN18	452	2288		TM	Extracellular
67	LG:340580.16:2002JAN18	2289	2311		TM	Transmembrane
67	LG:340580.16:2002JAN18	2312	2323		TM	Cytosolic
67	LG:340580.16:2002JAN18	2324	2346		TM	Transmembrane
67	LG:340580.16:2002JAN18	2347	2400		TM	Extracellular
67	LG:340580.16:2002JAN18	2401	2423		TM	Transmembrane
67	LG:340580.16:2002JAN18	2424	2446		TM	Cytosolic
67	LG:340580.16:2002JAN18	1	80		TM	Cytosolic
67	LG:340580.16:2002JAN18	81	103		TM	Transmembrane
67	LG:340580.16:2002JAN18	104	391		TM	Extracellular
67	LG:340580.16:2002JAN18	392	414		TM	Transmembrane
67	LG:340580.16:2002JAN18	415	426		TM	Cytosolic
67	LG:340580.16:2002JAN18	427	449		TM	Transmembrane
67	LG:340580.16:2002JAN18	450	1729		TM	Extracellular
67	LG:340580.16:2002JAN18	1730	1761		TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
67	LG:340580.16:2002JAN18	1762	1791		TM	Cytosolic
67	LG:340580.16:2002JAN18	1792	1814		TM	Transmembrane
67	LG:340580.16:2002JAN18	1815	1835		TM	Extracellular
67	LG:340580.16:2002JAN18	1836	1853		TM	Transmembrane
67	LG:340580.16:2002JAN18	1854	1873		TM	Cytosolic
67	LG:340580.16:2002JAN18	1874	1896		TM	Transmembrane
67	LG:340580.16:2002JAN18	1897	1979		TM	Extracellular
67	LG:340580.16:2002JAN18	1980	2002		TM	Transmembrane
67	LG:340580.16:2002JAN18	2003	2092		TM	Cytosolic
67	LG:340580.16:2002JAN18	2093	2115		TM	Transmembrane
67	LG:340580.16:2002JAN18	2116	2286		TM	Extracellular
67	LG:340580.16:2002JAN18	2287	2309		TM	Transmembrane
67	LG:340580.16:2002JAN18	2310	2321		TM	Cytosolic
67	LG:340580.16:2002JAN18	2322	2344		TM	Transmembrane
67	LG:340580.16:2002JAN18	2345	2363		TM	Extracellular
67	LG:340580.16:2002JAN18	2364	2386		TM	Transmembrane
67	LG:340580.16:2002JAN18	2387	2392		TM	Cytosolic
67	LG:340580.16:2002JAN18	2393	2415		TM	Transmembrane
67	LG:340580.16:2002JAN18	2416	2446		TM	Extracellular
67	LG:340580.16:2002JAN18	5926	5973	forward 1	SP	
67	LG:340580.16:2002JAN18	3085	3189	forward 1	SP	
67	LG:340580.16:2002JAN18	5926	5985	forward 1	SP	
67	LG:340580.16:2002JAN18	5926	6000	forward 1	SP	
67	LG:340580.16:2002JAN18	5926	6003	forward 1	SP	
67	LG:340580.16:2002JAN18	2573	2632	forward 2	SP	
67	LG:340580.16:2002JAN18	2573	2656	forward 2	SP	
67	LG:340580.16:2002JAN18	2573	2662	forward 2	SP	
67	LG:340580.16:2002JAN18	5187	5264	forward 3	SP	
67	LG:340580.16:2002JAN18	5202	5264	forward 3	SP	
67	LG:340580.16:2002JAN18	5187	5243	forward 3	SP	
67	LG:340580.16:2002JAN18	5187	5252	forward 3	SP	
67	LG:340580.16:2002JAN18	5187	5258	forward 3	SP	
67	LG:340580.16:2002JAN18	5187	5258	forward 3	SP	
68	LG:350272.6:2002JAN18	1	649		TM	Extracellular
68	LG:350272.6:2002JAN18	650	672		TM	Transmembrane
68	LG:350272.6:2002JAN18	673	679		TM	Cytosolic
68	LG:350272.6:2002JAN18	1967	2038	forward 2	SP	
68	LG:350272.6:2002JAN18	1832	1888	forward 2	SP	
68	LG:350272.6:2002JAN18	1967	2032	forward 2	SP	
68	LG:350272.6:2002JAN18	1967	2038	forward 2	SP	
68	LG:350272.6:2002JAN18	1967	2035	forward 2	SP	
68	LG:350272.6:2002JAN18	1793	1891	forward 2	SP	
68	LG:350272.6:2002JAN18	1967	2026	forward 2	SP	
68	LG:350272.6:2002JAN18	1787	1885	forward 2	SP	
68	LG:350272.6:2002JAN18	1218	1277	forward 3	SP	
68	LG:350272.6:2002JAN18	1218	1274	forward 3	SP	
68	LG:350272.6:2002JAN18	1218	1280	forward 3	SP	
69	LG:397228.1:2002JAN18	1	106		TM	Cytosolic
70	LG:401325.41:2002JAN18	1867	1959	forward 1	SP	

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
70	LG:401325.41:2002JAN18	2546	2617	forward 2	SP	
70	LG:401325.41:2002JAN18	2546	2611	forward 2	SP	
70	LG:401325.41:2002JAN18	2546	2617	forward 2	SP	
70	LG:401325.41:2002JAN18	2546	2596	forward 2	SP	
70	LG:401325.41:2002JAN18	2666	2722	forward 2	SP	
71	LG:402029.14:2002JAN18	1	207		TM	Extracellular
71	LG:402029.14:2002JAN18	208	230		TM	Transmembrane
71	LG:402029.14:2002JAN18	231	305		TM	Cytosolic
71	LG:402029.14:2002JAN18	306	325		TM	Transmembrane
71	LG:402029.14:2002JAN18	326	339		TM	Extracellular
71	LG:402029.14:2002JAN18	340	357		TM	Transmembrane
71	LG:402029.14:2002JAN18	358	369		TM	Cytosolic
71	LG:402029.14:2002JAN18	370	392		TM	Transmembrane
71	LG:402029.14:2002JAN18	393	1147		TM	Extracellular
71	LG:402029.14:2002JAN18	2527	2607	forward 1	SP	
71	LG:402029.14:2002JAN18	1342	1431	forward 1	SP	
72	LG:407233.2:2002JAN18	1	773		TM	Extracellular
72	LG:407233.2:2002JAN18	774	796		TM	Transmembrane
72	LG:407233.2:2002JAN18	797	798		TM	Cytosolic
72	LG:407233.2:2002JAN18	1	57		TM	Cytosolic
72	LG:407233.2:2002JAN18	58	80		TM	Transmembrane
72	LG:407233.2:2002JAN18	81	798		TM	Extracellular
72	LG:407233.2:2002JAN18	1	50		TM	Extracellular
72	LG:407233.2:2002JAN18	51	73		TM	Transmembrane
72	LG:407233.2:2002JAN18	74	390		TM	Cytosolic
72	LG:407233.2:2002JAN18	391	413		TM	Transmembrane
72	LG:407233.2:2002JAN18	414	689		TM	Extracellular
72	LG:407233.2:2002JAN18	690	712		TM	Transmembrane
72	LG:407233.2:2002JAN18	713	798		TM	Cytosolic
72	LG:407233.2:2002JAN18	1180	1266	forward 1	SP	
72	LG:407233.2:2002JAN18	139	213	forward 1	SP	
72	LG:407233.2:2002JAN18	1192	1257	forward 1	SP	
72	LG:407233.2:2002JAN18	1204	1266	forward 1	SP	
72	LG:407233.2:2002JAN18	1182	1265	forward 3	SP	
73	LG:407346.1:2002JAN18	1	519		TM	Extracellular
73	LG:407346.1:2002JAN18	520	542		TM	Transmembrane
73	LG:407346.1:2002JAN18	543	562		TM	Cytosolic
73	LG:407346.1:2002JAN18	563	585		TM	Transmembrane
73	LG:407346.1:2002JAN18	586	1725		TM	Extracellular
73	LG:407346.1:2002JAN18	1726	1748		TM	Transmembrane
73	LG:407346.1:2002JAN18	1749	2071		TM	Cytosolic
73	LG:407346.1:2002JAN18	2072	2094		TM	Transmembrane
73	LG:407346.1:2002JAN18	2095	2126		TM	Extracellular
73	LG:407346.1:2002JAN18	2127	2149		TM	Transmembrane
73	LG:407346.1:2002JAN18	2150	2161		TM	Cytosolic
73	LG:407346.1:2002JAN18	1	2001		TM	Extracellular
73	LG:407346.1:2002JAN18	2002	2021		TM	Transmembrane
73	LG:407346.1:2002JAN18	2022	2161		TM	Cytosolic
73	LG:407346.1:2002JAN18	1	1616		TM	Extracellular

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
73	LG:407346.1:2002JAN18	1617	1639		TM	Transmembrane
73	LG:407346.1:2002JAN18	1640	1741		TM	Cytosolic
73	LG:407346.1:2002JAN18	1742	1764		TM	Transmembrane
73	LG:407346.1:2002JAN18	1765	2161		TM	Extracellular
74	LG:407689.7:2002JAN18	1	2173		TM	Extracellular
74	LG:407689.7:2002JAN18	2174	2196		TM	Transmembrane
74	LG:407689.7:2002JAN18	2197	2202		TM	Cytosolic
74	LG:407689.7:2002JAN18	2203	2225		TM	Transmembrane
74	LG:407689.7:2002JAN18	2226	2259		TM	Extracellular
74	LG:407689.7:2002JAN18	2188	2262	forward 1	SP	
74	LG:407689.7:2002JAN18	4693	4752	forward 1	SP	
74	LG:407689.7:2002JAN18	2182	2262	forward 1	SP	
74	LG:407689.7:2002JAN18	2104	2181	forward 1	SP	
74	LG:407689.7:2002JAN18	1378	1458	forward 1	SP	
74	LG:407689.7:2002JAN18	2023	2094	forward 1	SP	
74	LG:407689.7:2002JAN18	4693	4755	forward 1	SP	
74	LG:407689.7:2002JAN18	6269	6331	forward 2	SP	
74	LG:407689.7:2002JAN18	1206	1274	forward 3	SP	
75	LG:407700.1:2002JAN18	1	20		TM	Cytosolic
75	LG:407700.1:2002JAN18	21	43		TM	Transmembrane
75	LG:407700.1:2002JAN18	44	750		TM	Extracellular
75	LG:407700.1:2002JAN18	1	571		TM	Extracellular
75	LG:407700.1:2002JAN18	572	594		TM	Transmembrane
75	LG:407700.1:2002JAN18	595	714		TM	Cytosolic
75	LG:407700.1:2002JAN18	715	737		TM	Transmembrane
75	LG:407700.1:2002JAN18	738	750		TM	Extracellular
75	LG:407700.1:2002JAN18	47	106	forward 2	SP	
75	LG:407700.1:2002JAN18	47	106	forward 2	SP	
75	LG:407700.1:2002JAN18	47	139	forward 2	SP	
75	LG:407700.1:2002JAN18	47	103	forward 2	SP	
75	LG:407700.1:2002JAN18	47	109	forward 2	SP	
75	LG:407700.1:2002JAN18	378	464	forward 3	SP	
76	LG:410461.92:2002JAN18	1	262		TM	Extracellular
76	LG:410461.92:2002JAN18	263	285		TM	Transmembrane
76	LG:410461.92:2002JAN18	286	492		TM	Cytosolic
76	LG:410461.92:2002JAN18	493	515		TM	Transmembrane
76	LG:410461.92:2002JAN18	516	950		TM	Extracellular
76	LG:410461.92:2002JAN18	258	344	forward 3	SP	
76	LG:410461.92:2002JAN18	258	344	forward 3	SP	
76	LG:410461.92:2002JAN18	258	338	forward 3	SP	
76	LG:410461.92:2002JAN18	273	344	forward 3	SP	
76	LG:410461.92:2002JAN18	273	338	forward 3	SP	
76	LG:410461.92:2002JAN18	258	338	forward 3	SP	
76	LG:410461.92:2002JAN18	276	338	forward 3	SP	
77	LG:411043.3:2002JAN18	1	121		TM	Cytosolic
77	LG:411043.3:2002JAN18	122	144		TM	Transmembrane
77	LG:411043.3:2002JAN18	145	203		TM	Extracellular
77	LG:411043.3:2002JAN18	204	223		TM	Transmembrane
77	LG:411043.3:2002JAN18	224	458		TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
77	LG:411043.3:2002JAN18	459	481		TM	Transmembrane
77	LG:411043.3:2002JAN18	482	707		TM	Extracellular
77	LG:411043.3:2002JAN18	606	668	forward 3	SP	
78	LG:438690.47:2002JAN18	1	1512		TM	Extracellular
78	LG:438690.47:2002JAN18	1513	1535		TM	Transmembrane
78	LG:438690.47:2002JAN18	1536	1767		TM	Cytosolic
78	LG:438690.47:2002JAN18	1768	1787		TM	Transmembrane
78	LG:438690.47:2002JAN18	1788	1788		TM	Extracellular
78	LG:438690.47:2002JAN18	1	1506		TM	Extracellular
78	LG:438690.47:2002JAN18	1507	1529		TM	Transmembrane
78	LG:438690.47:2002JAN18	1530	1662		TM	Cytosolic
78	LG:438690.47:2002JAN18	1663	1685		TM	Transmembrane
78	LG:438690.47:2002JAN18	1686	1788		TM	Extracellular
78	LG:438690.47:2002JAN18	3451	3522	forward 1	SP	
78	LG:438690.47:2002JAN18	1777	1866	forward 1	SP	
78	LG:438690.47:2002JAN18	3451	3522	forward 1	SP	
78	LG:438690.47:2002JAN18	3451	3525	forward 1	SP	
78	LG:438690.47:2002JAN18	3032	3085	forward 2	SP	
78	LG:438690.47:2002JAN18	3032	3091	forward 2	SP	
78	LG:438690.47:2002JAN18	1043	1120	forward 2	SP	
78	LG:438690.47:2002JAN18	3032	3100	forward 2	SP	
78	LG:438690.47:2002JAN18	582	650	forward 3	SP	
79	LG:444677.81:2002JAN18	1055	1111	forward 2	SP	
79	LG:444677.81:2002JAN18	818	880	forward 2	SP	
79	LG:444677.81:2002JAN18	234	293	forward 3	SP	
80	LG:457464.24:2002JAN18	1	438		TM	Extracellular
80	LG:457464.24:2002JAN18	439	461		TM	Transmembrane
80	LG:457464.24:2002JAN18	462	536		TM	Cytosolic
80	LG:457464.24:2002JAN18	1000	1092	forward 1	SP	
80	LG:457464.24:2002JAN18	1347	1400	forward 3	SP	
80	LG:457464.24:2002JAN18	1347	1403	forward 3	SP	
81	LG:7684793.15:2002JAN18	940	1002	forward 1	SP	
81	LG:7684793.15:2002JAN18	940	1008	forward 1	SP	
81	LG:7684793.15:2002JAN18	3253	3345	forward 1	SP	
81	LG:7684793.15:2002JAN18	3155	3244	forward 2	SP	
81	LG:7684793.15:2002JAN18	2117	2194	forward 2	SP	
81	LG:7684793.15:2002JAN18	2114	2188	forward 2	SP	
81	LG:7684793.15:2002JAN18	3984	4058	forward 3	SP	
82	LG:7687485.1:2002JAN18	1	252		TM	Cytosolic
82	LG:7687485.1:2002JAN18	253	275		TM	Transmembrane
82	LG:7687485.1:2002JAN18	276	380		TM	Extracellular
82	LG:7687485.1:2002JAN18	781	828	forward 1	SP	
82	LG:7687485.1:2002JAN18	781	834	forward 1	SP	
82	LG:7687485.1:2002JAN18	299	367	forward 2	SP	
82	LG:7687485.1:2002JAN18	299	361	forward 2	SP	
83	LG:7689661.4:2002JAN18	1	345		TM	Extracellular
83	LG:7689661.4:2002JAN18	346	365		TM	Transmembrane
83	LG:7689661.4:2002JAN18	366	509		TM	Cytosolic
83	LG:7689661.4:2002JAN18	510	532		TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
83	LG:7689661.4:2002JAN18	533	757		TM	Extracellular
83	LG:7689661.4:2002JAN18	1562	1618	forward 2	SP	
84	LG:7690373.1:2002JAN18	1	95		TM	Cytosolic
84	LG:7690373.1:2002JAN18	96	118		TM	Transmembrane
84	LG:7690373.1:2002JAN18	119	219		TM	Extracellular
85	LG:7696560.1:2002JAN18	1	556		TM	Extracellular
85	LG:7696560.1:2002JAN18	557	576		TM	Transmembrane
85	LG:7696560.1:2002JAN18	577	602		TM	Cytosolic
85	LG:7696560.1:2002JAN18	1135	1194	forward 1	SP	
85	LG:7696560.1:2002JAN18	83	166	forward 2	SP	
86	LG:7698190.26:2002JAN18	1	1466		TM	Extracellular
86	LG:7698190.26:2002JAN18	1467	1489		TM	Transmembrane
86	LG:7698190.26:2002JAN18	1490	1521		TM	Cytosolic
86	LG:7698190.26:2002JAN18	1	1460		TM	Extracellular
86	LG:7698190.26:2002JAN18	1461	1483		TM	Transmembrane
86	LG:7698190.26:2002JAN18	1484	1521		TM	Cytosolic
86	LG:7698190.26:2002JAN18	1	1465		TM	Extracellular
86	LG:7698190.26:2002JAN18	1466	1488		TM	Transmembrane
86	LG:7698190.26:2002JAN18	1489	1520		TM	Cytosolic
86	LG:7698190.26:2002JAN18	2872	2976	forward 1	SP	
86	LG:7698190.26:2002JAN18	4408	4470	forward 1	SP	
87	LG:7763560.12:2002JAN18	1162	1260	forward 1	SP	
87	LG:7763560.12:2002JAN18	2225	2308	forward 2	SP	
87	LG:7763560.12:2002JAN18	2225	2308	forward 2	SP	
88	LG:7763587.20:2002JAN18	431	523	forward 2	SP	
88	LG:7763587.20:2002JAN18	476	520	forward 2	SP	
88	LG:7763587.20:2002JAN18	476	550	forward 2	SP	
88	LG:7763587.20:2002JAN18	1692	1787	forward 3	SP	
89	LG:899263.10:2002JAN18	1	784		TM	Extracellular
89	LG:899263.10:2002JAN18	785	807		TM	Transmembrane
89	LG:899263.10:2002JAN18	808	911		TM	Cytosolic
89	LG:899263.10:2002JAN18	93	167	forward 3	SP	
90	LG:977837.31:2002JAN18	1	55		TM	Extracellular
90	LG:977837.31:2002JAN18	56	78		TM	Transmembrane
90	LG:977837.31:2002JAN18	79	84		TM	Cytosolic
90	LG:977837.31:2002JAN18	85	107		TM	Transmembrane
90	LG:977837.31:2002JAN18	108	320		TM	Extracellular
91	LG:978560.13:2002JAN18	1	1399		TM	Extracellular
91	LG:978560.13:2002JAN18	1400	1419		TM	Transmembrane
91	LG:978560.13:2002JAN18	1420	1426		TM	Cytosolic
91	LG:978560.13:2002JAN18	1	1396		TM	Extracellular
91	LG:978560.13:2002JAN18	1397	1419		TM	Transmembrane
91	LG:978560.13:2002JAN18	1420	1425		TM	Cytosolic
91	LG:978560.13:2002JAN18	2735	2806	forward 2	SP	
91	LG:978560.13:2002JAN18	3971	4039	forward 2	SP	
91	LG:978560.13:2002JAN18	3971	4033	forward 2	SP	
91	LG:978560.13:2002JAN18	2735	2809	forward 2	SP	
91	LG:978560.13:2002JAN18	2735	2806	forward 2	SP	
91	LG:978560.13:2002JAN18	3971	4030	forward 2	SP	

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
91	LG:978560.13:2002JAN18	3971	4033	forward 2	SP	
91	LG:978560.13:2002JAN18	3621	3677	forward 3	SP	
91	LG:978560.13:2002JAN18	3621	3665	forward 3	SP	
91	LG:978560.13:2002JAN18	579	650	forward 3	SP	
91	LG:978560.13:2002JAN18	558	650	forward 3	SP	
91	LG:978560.13:2002JAN18	579	656	forward 3	SP	
91	LG:978560.13:2002JAN18	558	656	forward 3	SP	
91	LG:978560.13:2002JAN18	558	656	forward 3	SP	
92	LG:979390.2:2002JAN18	886	948	forward 1	SP	
92	LG:979390.2:2002JAN18	861	938	forward 3	SP	
92	LG:979390.2:2002JAN18	543	605	forward 3	SP	
92	LG:979390.2:2002JAN18	861	953	forward 3	SP	
92	LG:979390.2:2002JAN18	543	614	forward 3	SP	
93	LG:983019.1:2002JAN18	1338	1397	forward 3	SP	
94	LG:997202.7:2002JAN18	1	1795		TM	Extracellular
94	LG:997202.7:2002JAN18	1796	1818		TM	Transmembrane
94	LG:997202.7:2002JAN18	1819	1837		TM	Cytosolic
94	LG:997202.7:2002JAN18	1838	1860		TM	Transmembrane
94	LG:997202.7:2002JAN18	1861	1869		TM	Extracellular
94	LG:997202.7:2002JAN18	1870	1892		TM	Transmembrane
94	LG:997202.7:2002JAN18	1893	2198		TM	Cytosolic
94	LG:997202.7:2002JAN18	3064	3162	forward 1	SP	
94	LG:997202.7:2002JAN18	3076	3153	forward 1	SP	
94	LG:997202.7:2002JAN18	4567	4626	forward 1	SP	
94	LG:997202.7:2002JAN18	4024	4095	forward 1	SP	
94	LG:997202.7:2002JAN18	3086	3148	forward 2	SP	
94	LG:997202.7:2002JAN18	3086	3157	forward 2	SP	
94	LG:997202.7:2002JAN18	3086	3154	forward 2	SP	
94	LG:997202.7:2002JAN18	3086	3163	forward 2	SP	
94	LG:997202.7:2002JAN18	3086	3163	forward 2	SP	
94	LG:997202.7:2002JAN18	6288	6332	forward 3	SP	
94	LG:997202.7:2002JAN18	738	794	forward 3	SP	
94	LG:997202.7:2002JAN18	6288	6347	forward 3	SP	
94	LG:997202.7:2002JAN18	6288	6347	forward 3	SP	
94	LG:997202.7:2002JAN18	1140	1214	forward 3	SP	
94	LG:997202.7:2002JAN18	1467	1577	forward 3	SP	
94	LG:997202.7:2002JAN18	1134	1214	forward 3	SP	
94	LG:997202.7:2002JAN18	5583	5672	forward 3	SP	
95	LG:998756.3:2002JAN18	1	57		TM	Cytosolic
95	LG:998756.3:2002JAN18	58	77		TM	Transmembrane
95	LG:998756.3:2002JAN18	78	80		TM	Extracellular
95	LG:998756.3:2002JAN18	81	103		TM	Transmembrane
95	LG:998756.3:2002JAN18	104	208		TM	Cytosolic
95	LG:998756.3:2002JAN18	209	231		TM	Transmembrane
95	LG:998756.3:2002JAN18	232	245		TM	Extracellular
95	LG:998756.3:2002JAN18	246	268		TM	Transmembrane
95	LG:998756.3:2002JAN18	269	297		TM	Cytosolic
95	LG:998756.3:2002JAN18	298	320		TM	Transmembrane
95	LG:998756.3:2002JAN18	321	1455		TM	Extracellular

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
95	LG:998756.3:2002JAN18	1	175		TM	Extracellular
95	LG:998756.3:2002JAN18	176	198		TM	Transmembrane
95	LG:998756.3:2002JAN18	199	204		TM	Cytosolic
95	LG:998756.3:2002JAN18	205	224		TM	Transmembrane
95	LG:998756.3:2002JAN18	225	1455		TM	Extracellular
95	LG:998756.3:2002JAN18	157	234	forward 1	SP	
95	LG:998756.3:2002JAN18	157	237	forward 1	SP	
95	LG:998756.3:2002JAN18	157	216	forward 1	SP	
95	LG:998756.3:2002JAN18	157	234	forward 1	SP	
95	LG:998756.3:2002JAN18	716	790	forward 2	SP	
95	LG:998756.3:2002JAN18	716	796	forward 2	SP	
95	LG:998756.3:2002JAN18	716	796	forward 2	SP	
95	LG:998756.3:2002JAN18	716	799	forward 2	SP	
95	LG:998756.3:2002JAN18	1461	1553	forward 3	SP	
95	LG:998756.3:2002JAN18	1461	1559	forward 3	SP	
96	LG:103460.28:2002JAN18	1	88		TM	Cytosolic
96	LG:103460.28:2002JAN18	89	111		TM	Transmembrane
96	LG:103460.28:2002JAN18	112	500		TM	Extracellular
96	LG:103460.28:2002JAN18	501	523		TM	Transmembrane
96	LG:103460.28:2002JAN18	524	663		TM	Cytosolic
96	LG:103460.28:2002JAN18	1	87		TM	Cytosolic
96	LG:103460.28:2002JAN18	88	105		TM	Transmembrane
96	LG:103460.28:2002JAN18	106	662		TM	Extracellular
96	LG:103460.28:2002JAN18	256	324	forward 1	SP	
96	LG:103460.28:2002JAN18	256	339	forward 1	SP	
96	LG:103460.28:2002JAN18	256	330	forward 1	SP	
96	LG:103460.28:2002JAN18	256	330	forward 1	SP	
96	LG:103460.28:2002JAN18	256	324	forward 1	SP	
96	LG:103460.28:2002JAN18	1029	1100	forward 3	SP	
97	LG:1501505.19:2002JAN18	1	48		TM	Cytosolic
97	LG:1501505.19:2002JAN18	49	71		TM	Transmembrane
97	LG:1501505.19:2002JAN18	72	80		TM	Extracellular
97	LG:1501505.19:2002JAN18	81	103		TM	Transmembrane
97	LG:1501505.19:2002JAN18	104	109		TM	Cytosolic
97	LG:1501505.19:2002JAN18	110	132		TM	Transmembrane
97	LG:1501505.19:2002JAN18	133	368		TM	Extracellular
98	LG:233444.9:2002JAN18	1	33		TM	Cytosolic
98	LG:233444.9:2002JAN18	34	56		TM	Transmembrane
98	LG:233444.9:2002JAN18	57	681		TM	Extracellular
98	LG:233444.9:2002JAN18	682	704		TM	Transmembrane
98	LG:233444.9:2002JAN18	705	723		TM	Cytosolic
98	LG:233444.9:2002JAN18	724	746		TM	Transmembrane
98	LG:233444.9:2002JAN18	747	911		TM	Extracellular
98	LG:233444.9:2002JAN18	1	69		TM	Cytosolic
98	LG:233444.9:2002JAN18	70	89		TM	Transmembrane
98	LG:233444.9:2002JAN18	90	103		TM	Extracellular
98	LG:233444.9:2002JAN18	104	126		TM	Transmembrane
98	LG:233444.9:2002JAN18	127	138		TM	Cytosolic
98	LG:233444.9:2002JAN18	139	161		TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
98	LG:233444.9:2002JAN18	162	194		TM	Extracellular
98	LG:233444.9:2002JAN18	195	217		TM	Transmembrane
98	LG:233444.9:2002JAN18	218	237		TM	Cytosolic
98	LG:233444.9:2002JAN18	238	260		TM	Transmembrane
98	LG:233444.9:2002JAN18	261	274		TM	Extracellular
98	LG:233444.9:2002JAN18	275	297		TM	Transmembrane
98	LG:233444.9:2002JAN18	298	430		TM	Cytosolic
98	LG:233444.9:2002JAN18	431	453		TM	Transmembrane
98	LG:233444.9:2002JAN18	454	472		TM	Extracellular
98	LG:233444.9:2002JAN18	473	495		TM	Transmembrane
98	LG:233444.9:2002JAN18	496	671		TM	Cytosolic
98	LG:233444.9:2002JAN18	672	694		TM	Transmembrane
98	LG:233444.9:2002JAN18	695	761		TM	Extracellular
98	LG:233444.9:2002JAN18	762	784		TM	Transmembrane
98	LG:233444.9:2002JAN18	785	802		TM	Cytosolic
98	LG:233444.9:2002JAN18	803	825		TM	Transmembrane
98	LG:233444.9:2002JAN18	826	910		TM	Extracellular
98	LG:233444.9:2002JAN18	1	194		TM	Extracellular
98	LG:233444.9:2002JAN18	195	217		TM	Transmembrane
98	LG:233444.9:2002JAN18	218	228		TM	Cytosolic
98	LG:233444.9:2002JAN18	229	251		TM	Transmembrane
98	LG:233444.9:2002JAN18	252	801		TM	Extracellular
98	LG:233444.9:2002JAN18	802	824		TM	Transmembrane
98	LG:233444.9:2002JAN18	825	910		TM	Cytosolic
99	LG:234824.7:2002JAN18	1	1193		TM	Extracellular
99	LG:234824.7:2002JAN18	1194	1216		TM	Transmembrane
99	LG:234824.7:2002JAN18	1217	1227		TM	Cytosolic
99	LG:234824.7:2002JAN18	1228	1250		TM	Transmembrane
99	LG:234824.7:2002JAN18	1251	1253		TM	Extracellular
99	LG:234824.7:2002JAN18	1254	1273		TM	Transmembrane
99	LG:234824.7:2002JAN18	1274	1279		TM	Cytosolic
99	LG:234824.7:2002JAN18	1280	1302		TM	Transmembrane
99	LG:234824.7:2002JAN18	1303	1942		TM	Extracellular
99	LG:234824.7:2002JAN18	1943	1965		TM	Transmembrane
99	LG:234824.7:2002JAN18	1966	1984		TM	Cytosolic
99	LG:234824.7:2002JAN18	1	1945		TM	Extracellular
99	LG:234824.7:2002JAN18	1946	1968		TM	Transmembrane
99	LG:234824.7:2002JAN18	1969	1984		TM	Cytosolic
99	LG:234824.7:2002JAN18	1	1936		TM	Extracellular
99	LG:234824.7:2002JAN18	1937	1956		TM	Transmembrane
99	LG:234824.7:2002JAN18	1957	1984		TM	Cytosolic
99	LG:234824.7:2002JAN18	2337	2408	forward 3	SP	
99	LG:234824.7:2002JAN18	2337	2390	forward 3	SP	
99	LG:234824.7:2002JAN18	2508	2579	forward 3	SP	
99	LG:234824.7:2002JAN18	2721	2822	forward 3	SP	
99	LG:234824.7:2002JAN18	4626	4676	forward 3	SP	
99	LG:234824.7:2002JAN18	2508	2582	forward 3	SP	
100	LG:235708.23:2002JAN18	1	67		TM	Extracellular
100	LG:235708.23:2002JAN18	68	90		TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
100	LG:235708.23:2002JAN18	91	101		TM	Cytosolic
100	LG:235708.23:2002JAN18	102	124		TM	Transmembrane
100	LG:235708.23:2002JAN18	125	1270		TM	Extracellular
101	LG:236649.14:2002JAN18	1	457		TM	Extracellular
101	LG:236649.14:2002JAN18	458	480		TM	Transmembrane
101	LG:236649.14:2002JAN18	481	492		TM	Cytosolic
101	LG:236649.14:2002JAN18	493	515		TM	Transmembrane
101	LG:236649.14:2002JAN18	516	529		TM	Extracellular
101	LG:236649.14:2002JAN18	530	552		TM	Transmembrane
101	LG:236649.14:2002JAN18	553	604		TM	Cytosolic
101	LG:236649.14:2002JAN18	1	391		TM	Extracellular
101	LG:236649.14:2002JAN18	392	414		TM	Transmembrane
101	LG:236649.14:2002JAN18	415	455		TM	Cytosolic
101	LG:236649.14:2002JAN18	456	478		TM	Transmembrane
101	LG:236649.14:2002JAN18	479	539		TM	Extracellular
101	LG:236649.14:2002JAN18	540	562		TM	Transmembrane
101	LG:236649.14:2002JAN18	563	603		TM	Cytosolic
101	LG:236649.14:2002JAN18	1	392		TM	Cytosolic
101	LG:236649.14:2002JAN18	393	415		TM	Transmembrane
101	LG:236649.14:2002JAN18	416	454		TM	Extracellular
101	LG:236649.14:2002JAN18	455	477		TM	Transmembrane
101	LG:236649.14:2002JAN18	478	603		TM	Cytosolic
102	LG:332474.7:2002JAN18	1	300		TM	Cytosolic
102	LG:332474.7:2002JAN18	301	320		TM	Transmembrane
102	LG:332474.7:2002JAN18	321	321		TM	Extracellular
102	LG:332474.7:2002JAN18	892	963	forward 1	SP	
102	LG:332474.7:2002JAN18	429	494	forward 3	SP	
102	LG:332474.7:2002JAN18	429	482	forward 3	SP	
102	LG:332474.7:2002JAN18	429	512	forward 3	SP	
102	LG:332474.7:2002JAN18	429	491	forward 3	SP	
102	LG:332474.7:2002JAN18	429	488	forward 3	SP	
103	LG:335727.8:2002JAN18	1	346		TM	Extracellular
103	LG:335727.8:2002JAN18	347	369		TM	Transmembrane
103	LG:335727.8:2002JAN18	370	377		TM	Cytosolic
103	LG:335727.8:2002JAN18	1	214		TM	Extracellular
103	LG:335727.8:2002JAN18	215	237		TM	Transmembrane
103	LG:335727.8:2002JAN18	238	341		TM	Cytosolic
103	LG:335727.8:2002JAN18	342	360		TM	Transmembrane
103	LG:335727.8:2002JAN18	361	377		TM	Extracellular
103	LG:335727.8:2002JAN18	25	90	forward 1	SP	
104	LG:481983.1:2002JAN18	1	19		TM	Extracellular
104	LG:481983.1:2002JAN18	20	42		TM	Transmembrane
104	LG:481983.1:2002JAN18	43	450		TM	Cytosolic
104	LG:481983.1:2002JAN18	451	469		TM	Transmembrane
104	LG:481983.1:2002JAN18	470	488		TM	Extracellular
104	LG:481983.1:2002JAN18	489	511		TM	Transmembrane
104	LG:481983.1:2002JAN18	512	571		TM	Cytosolic
104	LG:481983.1:2002JAN18	572	594		TM	Transmembrane
104	LG:481983.1:2002JAN18	595	603		TM	Extracellular

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
104	LG:481983.1:2002JAN18	604	626		TM	Transmembrane
104	LG:481983.1:2002JAN18	627	928		TM	Cytosolic
104	LG:481983.1:2002JAN18	929	951		TM	Transmembrane
104	LG:481983.1:2002JAN18	952	1382		TM	Extracellular
104	LG:481983.1:2002JAN18	1383	1405		TM	Transmembrane
104	LG:481983.1:2002JAN18	1406	1611		TM	Cytosolic
104	LG:481983.1:2002JAN18	1612	1634		TM	Transmembrane
104	LG:481983.1:2002JAN18	1635	2147		TM	Extracellular
104	LG:481983.1:2002JAN18	2148	2170		TM	Transmembrane
104	LG:481983.1:2002JAN18	2171	2271		TM	Cytosolic
104	LG:481983.1:2002JAN18	1	36		TM	Extracellular
104	LG:481983.1:2002JAN18	37	59		TM	Transmembrane
104	LG:481983.1:2002JAN18	60	159		TM	Cytosolic
104	LG:481983.1:2002JAN18	160	179		TM	Transmembrane
104	LG:481983.1:2002JAN18	180	188		TM	Extracellular
104	LG:481983.1:2002JAN18	189	206		TM	Transmembrane
104	LG:481983.1:2002JAN18	207	243		TM	Cytosolic
104	LG:481983.1:2002JAN18	244	266		TM	Transmembrane
104	LG:481983.1:2002JAN18	267	280		TM	Extracellular
104	LG:481983.1:2002JAN18	281	303		TM	Transmembrane
104	LG:481983.1:2002JAN18	304	447		TM	Cytosolic
104	LG:481983.1:2002JAN18	448	470		TM	Transmembrane
104	LG:481983.1:2002JAN18	471	927		TM	Extracellular
104	LG:481983.1:2002JAN18	928	950		TM	Transmembrane
104	LG:481983.1:2002JAN18	951	969		TM	Cytosolic
104	LG:481983.1:2002JAN18	970	992		TM	Transmembrane
104	LG:481983.1:2002JAN18	993	1160		TM	Extracellular
104	LG:481983.1:2002JAN18	1161	1183		TM	Transmembrane
104	LG:481983.1:2002JAN18	1184	1216		TM	Cytosolic
104	LG:481983.1:2002JAN18	1217	1239		TM	Transmembrane
104	LG:481983.1:2002JAN18	1240	2271		TM	Extracellular
104	LG:481983.1:2002JAN18	1465	1524	forward 1	SP	
104	LG:481983.1:2002JAN18	1465	1518	forward 1	SP	
104	LG:481983.1:2002JAN18	1465	1509	forward 1	SP	
104	LG:481983.1:2002JAN18	3116	3160	forward 2	SP	
104	LG:481983.1:2002JAN18	1271	1345	forward 2	SP	
104	LG:481983.1:2002JAN18	1271	1351	forward 2	SP	
104	LG:481983.1:2002JAN18	570	626	forward 3	SP	
104	LG:481983.1:2002JAN18	831	905	forward 3	SP	
104	LG:481983.1:2002JAN18	1833	1892	forward 3	SP	

TABLE 5

SEQ ID NO:/Template ID	Component Span
1/LG:1447398.9:2002JAN18	1513-1947; 1446-1810; 1232-1808; 1394-1805; 1349-1804; 1338-1800; 1394-1800; 1575-1770; 1424-1798; 1540-1780; 1321-1619; 1313-1610; 1232-1482; 993-1458; 1159-1447; 1024-1415; 1174-1389; 998-1286; 601-1232; 836-1212; 724-1168; 905-1163; 706-1161; 798-1161; 909-1161; 914-1161;927-1161; 777-1161; 746-1160; 739-1153; 646-1100; 662-1100; 627-1100; 693-1100; 715-1100; 628-1100; 663-1100; 563-1082; 492-1077; 888-1066; 717-1062; 635-990; 562-907; 502-903; 580-815; 1-624; 194-484
2/LG:201488.3:2002JAN18	1-226; 75-328; 77-245; 176-447; 245-319; 270-319; 278-616; 291-535; 296-784; 351-630; 351-551; 354-936; 474-578; 539-792; 556-905; 610-853; 613-874; 613-864; 616-857; 659-891; 664-785; 676-1210; 714-967; 720-1281; 734-992; 736-786; 744-1344; 749-899; 760-1023; 817-979; 839-1111; 847-1117; 864-1318; 888-1581; 896-1438; 904-1203; 918-1182; 923-1202; 947-1050; 987-1567; 1035-1116; 1059-1527; 1081-1228; 1088-1292; 1085-1476; 1107-1351; 1109-1355; 1125-1627; 1126-1578; 1129-1578; 1126-1220; 1156-1558; 1147-1581; 1161-1581; 1160-1356; 1164-1578; 1167-1329; 1169-1577; 1173-1565; 1177-1575; 1192-1460; 1193-1544; 1205-1577; 1205-1599; 1206-1580; 1207-1577; 1208-1577; 1213-1587; 1211-1452; 1215-1572; 1234-1577; 1236-1577; 1236-1434; 1242-1503; 1244-1623; 1251-1577; 1262-1503; 1274-1577; 1277-1512; 1280-1586; 1284-1733; 1292-1568; 1305-1575; 1312-1577; 1325-1528; 1332-1578; 1353-1578; 1359-1580; 1362-1628; 1364-1507; 1364-1577; 1387-1581; 1392-1625; 1420-1581; 1459-1571; 1497-1577; 1586-1857
3/LG:288410.6:2002JAN18	1-605; 1-661; 1-486; 42-728; 657-1099; 770-1429; 1138-1529; 1405-2025; 1781-1996; 1907-2140; 1907-2317
4/LG:7682817.1:2002JAN18	1-201; 105-380; 123-607; 463-1099; 463-720; 786-1090; 971-1128; 1012-1516; 1141-1560
5/LG:7685059.6:2002JAN18	1-206; 1-361; 1-263; 36-474; 38-301; 42-307; 63-432; 49-668; 52-363; 52-148; 67-199; 81-662; 76-670; 76-431; 76-320; 76-303; 76-302; 103-368; 110-375; 119-410; 219-386; 218-763; 218-766; 321-560; 440-704
6/LG:7689671.1:2002JAN18	1-451; 1-256; 308-901; 308-557; 308-830; 312-387
7/LG:7689684.1:2002JAN18	1-224; 1-61; 12-96; 111-474; 111-398; 123-518; 123-512; 126-358; 257-609; 305-364
8/LG:7762669.1:2002JAN18	1-255; 1-292; 18-458
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TABLE 5

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	2169-2358,2180-2493,2184-2358,2184-2844,2199-2844,2227-2326,2227-2431,2233-2369,2238-2700,2247-2788,2260-2330,2264-2907,2278-2829,2298-2814,2299-2892,2304-2776,2306-2824,2319-2508,2322-2876,2323-2604,2346-2630,2352-2572,2353-2507,2353-2679,2355-2520,2361-2531,2361-2811,2361-2822,2361-2842,2361-2869,2361-2870,2361-2929,2363-2877,2363-2941,2363-2950,2363-2954,2364-2507,2366-2950,2367-2859,2367-2937,2368-2863,2370-2762,2372-2662,2374-2671,2376-2580,2378-2973,2386-2653,2391-2616,2392-2507,2392-2663,2392-2920,2394-2742,2394-2961,2395-3022,2397-2746,2399-2634,2399-2668,2411-2565,2411-2647,2411-2656,2411-2672,2411-2674,2411-2721,2411-2742,2411-2766,2411-2805,2411-2808,2411-2811,2411-2832,2411-2839,2411-2842,2411-2883,2415-2812,2419-2587,2421-2684,2425-2644,2434-2990,2437-2555,2439-2570,2439-2991,2445-2740,2445-2743,2448-2688,2473-2855,2475-3021,2476-2635,2476-2762,2482-2855,2484-2762,2486-3124,2491-2801,2509-2992,2514-2750,2517-2780,2517-2992,2518-2825,2522-2891,2524-2967,2525-2612,2526-2800,2532-2771,2534-2689,2535-2778,2535-2847,

TABLE 5

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11/LG:018258.1:2002JAN18	1-622,5-837,83-256,126-378,126-393,265-497,265-736,309-614,500-657
12/LG:027320.5:2002JAN18	1-778,62-306,62-513,66-317,94-477,235-747,384-751,401-633,543-979,598-777,718-1399,859-1151,879-1299,880-1432,925-1274,946-1240,958-1379,963-1554,1036-1323,1093-1783,1111-1384,1359-2067,1720-2003,1950-2483,1973-2440,2041-2438,2240-2757,2242-2491,2362-2880,2362-2953,2409-2959,2724-2965,2875-3145,2881-3220,3101-3269
13/LG:057499.1:2002JAN18	1-1833,1010-1528,1041-1533,1049-1582,1061-1311,1086-1468,1106-1795,1154-1460,1186-1497,1199-1750,1206-1444,1225-1499,1225-1807,1239-1442,1277-1576,1278-1801,1334-1795,1374-1578,1377-1793,1394-1833,1406-1479,1417-1795,1419-1827,1433-1646,1450-1831,1471-1827,1476-1828,1523-1833,1535-1827,1540-1772,1540-1827,1561-1827,1584-1827,1615-1827,1624-1830,1627-1778,1672-2068,1674-1831,1680-1939,1695-1827,1778-2484,1860-2009,1874-2078,1876-2178,1895-2252,1898-2160,1981-2322,2006-2262,2030-2377,2082-2364,2099-2289,2099-2491,2124-2565,2124-2575,2133-2565,2160-2502,2172-2437,2173-2306,2180-3004,2227-2573,2246-2868,2283-2697,2284-2676,2287-2491,2287-2655,2288-2642,2290-2563,2327-2582,2346-2898,2357-2561,2369-2605,2399-2655,2410-2971,2412-3173,2416-2863,2434-2741,2434-2881,2446-2706,2552-2887,2566-3159,2587-2905,2604-2855,2607-2878,2614-2870,2634-3212,2658-2925,2662-2930,2719-3007,2752-3173,2813-3126,2815-3079,2816-3076,2824-3065,2842-3197,2848-3610,2862-3459,2870-3004,2907-3496,2920-3222,2944-3273,2964-3141,2991-3353,3049-3523,3060-3538,

TABLE 5

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TABLE 5

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17/LG:098580.3:2002JAN18	1-487,266-732,269-558,285-752,427-525
18/LG:1001879.1:2002JAN18	1330-1568; 1090-1557; 1134-1558; 968-1558; 1351-1528; 660-1244; 241-792; 63-758; 102-692; 241-632; 22-580; 1-292

TABLE 5

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	2397-2709; 2502-2577; 2526-2578
21/LG:1090358.10:2002JAN18	1-573; 2-279; 346-572; 354-564; 354-543; 410-1047; 530-788; 530-1118; 530-1047;527-1079; 546-860; 568-1064; 592-1002; 665-1118; 683-968; 689-1118; 691-1123; 700-1121; 703-1313; 702-1108; 721-1333; 754-1118; 861-1118; 861-1076; 866-937; 924-1018; 1123-1555; 1129-1793; 1504-2200; 1552-1778; 1555-1745; 1720-2099

TABLE 5

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23/LG:1099945.26:2002JAN18	1-415; 1-537; 182-535; 181-512; 182-533; 184-533; 187-612; 185-531; 187-533; 189-533; 192-521; 194-531; 195-532; 197-403; 197-521; 198-538; 202-533; 202-531; 208-533; 208-530; 211-533; 214-540; 214-533; 215-533; 215-540; 216-510; 216-540; 217-540; 217-533; 218-535; 218-533; 219-541; 219-533; 220-532; 220-533; 219-532; 222-540; 221-533; 221-530; 221-531; 221-540; 222-533; 222-541; 226-566; 224-533; 225-540; 225-536; 225-528; 227-533; 227-510; 226-538; 228-533; 228-515; 227-540; 228-540; 228-536; 228-541; 229-533; 228-534; 230-528; 230-558; 230-537; 230-533; 231-538; 232-541; 231-532; 233-536; 233-532; 234-533; 236-533; 237-533; 236-532; 237-540; 237-539; 238-533; 239-533; 239-532; 240-523; 241-540; 242-533; 241-533; 242-522; 243-532; 243-511; 242-510; 245-544; 244-510; 245-515; 246-533; 246-519; 249-508; 247-533; 247-540; 249-542; 249-531; 249-521; 249-500; 250-541; 250-533; 250-532; 252-541; 250-523; 250-520; 252-519; 254-542; 253-533; 254-533; 254-524; 254-487; 256-533; 257-533; 256-515; 257-507; 257-495; 257-497; 258-533; 258-497; 259-532; 261-538; 263-528; 264-506; 265-533; 265-531; 264-533; 266-532; 266-533; 266-511; 267-533; 267-518; 267-512;

TABLE 5

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TABLE 5

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TABLE 5

SEQ ID NO:/Template ID	Component Span
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103/LG:335727.8:2002JAN18	1-376; 34-461; 34-273; 34-257; 36-316; 38-304; 38-202; 41-149; 46-481; 52-316; 52-222; 65-578; 65-618; 65-396; 65-277; 67-267; 67-327; 73-567; 73-329; 73-181; 85-263; 88-718; 149-396; 170-554; 171-723; 175-723; 224-754; 224-433; 245-940; 319-554; 320-679; 440-671; 550-1073; 800-1133

TABLE 5

SEQ ID NO:/Template ID	Component Span
104/LG:481983.1:2002JAN18	1-615; 1-645; 1-644; 73-645; 571-930; 571-805; 642-905; 645-843; 677-1021; 797-1071; 797-1069; 824-1028; 860-1167; 909-1510; 970-1225; 972-1380; 987-1559; 1005-1622; 1066-1581; 1069-1614; 1077-1623; 1117-1527; 1117-1260; 1139-1551; 1152-1577; 1181-1357; 1194-1382; 1229-1687; 1268-1542; 1291-1723; 1293-1722; 1303-1709; 1312-1747; 1322-1691; 1356-1730; 1392-1655; 1394-1595; 1411-1585; 1411-1724; 1411-1683; 1411-1681; 1418-1688; 1510-1724; 1552-1672; 1587-1719; 1609-1849; 1640-1845; 1652-2103; 1760-1973; 1785-2230; 1902-2226; 2060-2682; 2100-2581; 2322-2821; 2469-2776; 2479-3028; 2598-3092; 2639-2925; 2708-3251; 3026-3300; 3043-3799; 3072-3342; 3113-3669; 3186-3434; 3399-3547; 3415-3630; 3416-3658; 3421-3815; 3440-3686; 3441-3919; 3455-3919; 3468-3787; 3478-3743; 3502-3786; 3563-3801; 3563-4115; 3632-4139; 3632-3825; 3632-3892; 3676-4183; 3651-3888; 3676-4126; 3680-3991; 3684-3951; 3695-3807; 3747-4143; 3749-4260; 3801-4255; 3801-4012; 3833-3994; 3861-4142; 3900-4238; 3905-4107; 3910-4521; 3912-4156; 3951-4414; 3994-4256; 4032-4606; 4040-4813; 4079-4423; 4115-4405; 4124-4265; 4128-4727; 4184-4458; 4197-4639; 4200-4567;
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TABLE 5

SEQ ID NO:/Template ID	Component Span
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TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
1	LG:1447398.9:2002JAN18	Germ Cells - 42%, Skin - 28%
2	LG:201488.3:2002JAN18	Female Genitalia - 13%, Cardiovascular System - 12%, Unclassified/Mixed - 11%
3	LG:288410.6:2002JAN18	Urinary Tract - 33%, Male Genitalia - 22%, Endocrine System - 22%
4	LG:7682817.1:2002JAN18	Cardiovascular System - 33%, Hemic and Immune System - 25%, Exocrine Glands - 25%
5	LG:7685059.6:2002JAN18	Liver - 27%, Skin - 23%, Hemic and Immune System - 15%, Endocrine System - 15%
6	LG:7689671.1:2002JAN18	Digestive System - 75%, Nervous System - 25%
7	LG:7689684.1:2002JAN18	Digestive System - 30%, Hemic and Immune System - 30%, Male Genitalia - 20%, Female Genitalia -
8	LG:7762669.1:2002JAN18	Pancreas - 82%, Digestive System - 18%
9	LG:965822.1:2002JAN18	Skin - 43%, Sense Organs - 29%, Germ Cells - 19%
10	LG:006394.31:2002JAN18	Sense Organs - 15%, Digestive System - 14%, Germ Cells - 13%
11	LG:018258.1:2002JAN18	Urinary Tract - 43%, Endocrine System - 29%, Digestive System - 21%
12	LG:027320.5:2002JAN18	Germ Cells - 33%, Embryonic Structures - 18%
13	LG:057499.1:2002JAN18	Skin - 13%
14	LG:065935.21:2002JAN18	Stomatognathic System - 30%, Unclassified/Mixed - 13%
15	LG:071860.12:2002JAN18	Exocrine Glands - 35%, Unclassified/Mixed - 25%, Endocrine System - 20%
16	LG:087383.29:2002JAN18	Sense Organs - 24%, Embryonic Structures - 16%
17	LG:098580.3:2002JAN18	Unclassified/Mixed - 38%, Cardiovascular System - 31%, Endocrine System - 31%
18	LG:1001879.1:2002JAN18	Unclassified/Mixed - 38%, Hemic and Immune System - 23%, Nervous System - 23%
19	LG:1079456.4:2002JAN18	Liver - 35%, Musculoskeletal System - 30%, Endocrine System - 20%
20	LG:1080598.9:2002JAN18	Germ Cells - 21%, Embryonic Structures - 15%
21	LG:1090358.10:2002JAN18	Liver - 25%, Embryonic Structures - 18%, Pancreas - 11%
22	LG:1097492.2:2002JAN18	Urinary Tract - 10%
23	LG:1099945.26:2002JAN18	Musculoskeletal System - 13%, Germ Cells - 11%
24	LG:110016.1:2002JAN18	Musculoskeletal System - 53%, Embryonic Structures - 12%
25	LG:1137613.10:2002JAN18	widely distributed
26	LG:118836.26:2002JAN18	Endocrine System - 13%, Connective Tissue - 12%, Hemic and Immune System - 10%
27	LG:1330261.32:2002JAN18	Male Genitalia - 17%, Cardiovascular System - 14%, Female Genitalia - 13%
28	LG:1347461.28:2002JAN18	Unclassified/Mixed - 29%, Hemic and Immune System - 11%
29	LG:1383494.16:2002JAN18	Sense Organs - 12%, Liver - 11%
30	LG:1400155.1:2002JAN18	Urinary Tract - 14%, Unclassified/Mixed - 10%
31	LG:1446621.1:2002JAN18	Endocrine System - 63%, Urinary Tract - 16%, Female Genitalia - 11%, Nervous System - 11%
32	LG:144920.1:2002JAN18	Liver - 23%, Unclassified/Mixed - 17%, Respiratory System - 15%

TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
33	LG:1452619.1:2002JAN18	widely distributed
34	LG:1453417.6:2002JAN18	Nervous System - 26%, Skin - 16%, Female Genitalia - 13%
35	LG:148485.8:2002JAN18	Sense Organs - 16%
36	LG:1502670.1:2002JAN18	Cardiovascular System - 15%, Endocrine System - 12%
37	LG:206593.3:2002JAN18	Exocrine Glands - 25%, Unclassified/Mixed - 18%, Nervous System - 14%, Endocrine System - 14%
38	LG:228273.22:2002JAN18	Nervous System - 16%, Unclassified/Mixed - 15%, Embryonic Structures - 11%
39	LG:228319.2:2002JAN18	Musculoskeletal System - 33%, Male Genitalia - 22%, Hemic and Immune System - 22%
40	LG:229165.16:2002JAN18	Unclassified/Mixed - 28%, Skin - 21%, Exocrine Glands - 11%
41	LG:230895.9:2002JAN18	Unclassified/Mixed - 40%, Respiratory System - 20%, Nervous System - 20%
42	LG:233552.5:2002JAN18	Germ Cells - 18%
43	LG:234430.7:2002JAN18	Sense Organs - 19%, Nervous System - 19%
44	LG:236659.1:2002JAN18	Unclassified/Mixed - 12%
45	LG:236767.26:2002JAN18	Musculoskeletal System - 18%, Sense Organs - 16%
46	LG:237489.7:2002JAN18	Pancreas - 36%, Respiratory System - 23%, Urinary Tract - 12%, Skin - 12%
47	LG:238218.20:2002JAN18	Liver - 10%
48	LG:239939.14:2002JAN18	Germ Cells - 32%, Connective Tissue - 11%, Nervous System - 11%
49	LG:242288.11:2002JAN18	Pancreas - 12%
50	LG:242491.29:2002JAN18	Sense Organs - 24%, Digestive System - 12%, Liver - 10%
51	LG:243488.41:2002JAN18	Male Genitalia - 17%, Endocrine System - 11%
52	LG:247792.18:2002JAN18	Sense Organs - 24%
53	LG:253193.17:2002JAN18	Pancreas - 39%, Hemic and Immune System - 24%, Embryonic Structures - 11%
54	LG:257088.20:2002JAN18	Unclassified/Mixed - 14%, Digestive System - 11%
55	LG:265552.1:2002JAN18	Sense Organs - 48%, Digestive System - 31%, Exocrine Glands - 10%
56	LG:275355.12:2002JAN18	Musculoskeletal System - 20%, Exocrine Glands - 18%, Female Genitalia - 14%
57	LG:280014.1:2002JAN18	Skin - 55%, Musculoskeletal System - 27%, Digestive System - 14%
58	LG:299937.3:2002JAN18	Stomatognathic System - 14%, Embryonic Structures - 11%
59	LG:311197.3:2002JAN18	Skin - 30%, Digestive System - 17%, Pancreas - 12%
60	LG:321069.2:2002JAN18	Stomatognathic System - 14%, Germ Cells - 13%, Urinary Tract - 12%
61	LG:330900.8:2002JAN18	Germ Cells - 16%, Hemic and Immune System - 11%
62	LG:330931.9:2002JAN18	Unclassified/Mixed - 12%, Embryonic Structures - 12%, Male Genitalia - 11%
63	LG:330985.1:2002JAN18	Germ Cells - 21%, Unclassified/Mixed - 15%
64	LG:332027.9:2002JAN18	Sense Organs - 21%, Liver - 13%

TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
65	LG:335377.8:2002JAN18	Unclassified/Mixed - 24%, Nervous System - 22%, Male Genitalia - 19%
66	LG:337452.25:2002JAN18	Germ Cells - 36%, Male Genitalia - 12%
67	LG:340580.16:2002JAN18	Female Genitalia - 11%
68	LG:350272.6:2002JAN18	Embryonic Structures - 13%, Musculoskeletal System - 12%
69	LG:397228.1:2002JAN18	Unclassified/Mixed - 42%, Cardiovascular System - 33%, Male Genitalia - 17%
70	LG:401325.41:2002JAN18	Nervous System - 19%, Skin - 12%, Unclassified/Mixed - 10%
71	LG:402029.14:2002JAN18	Respiratory System - 17%, Male Genitalia - 15%, Digestive System - 13%
72	LG:407233.2:2002JAN18	Endocrine System - 28%, Hemic and Immune System - 24%, Skin - 21%
73	LG:407346.1:2002JAN18	Sense Organs - 29%, Nervous System - 26%, Hemic and Immune System - 11%
74	LG:407689.7:2002JAN18	Digestive System - 14%, Nervous System - 11%, Hemic and Immune System - 11%
75	LG:407700.1:2002JAN18	Skin - 21%, Digestive System - 10%
76	LG:410461.92:2002JAN18	Musculoskeletal System - 19%, Liver - 19%, Endocrine System - 18%
77	LG:411043.3:2002JAN18	Pancreas - 16%, Exocrine Glands - 12%, Nervous System - 12%
78	LG:438690.47:2002JAN18	widely distributed
79	LG:444677.81:2002JAN18	Sense Organs - 31%, Urinary Tract - 15%, Skin - 12%, Male Genitalia - 12%
80	LG:457464.24:2002JAN18	Skin - 13%, Hemic and Immune System - 10%
81	LG:7684793.15:2002JAN18	Skin - 15%, Germ Cells - 10%
82	LG:7687485.1:2002JAN18	Cardiovascular System - 26%, Musculoskeletal System - 26%, Urinary Tract - 14%
83	LG:7689661.4:2002JAN18	Musculoskeletal System - 28%, Urinary Tract - 11%, Nervous System - 10%, Endocrine System - 10%
84	LG:7690373.1:2002JAN18	Male Genitalia - 40%, Nervous System - 40%, Hemic and Immune System - 20%
85	LG:7696560.1:2002JAN18	Nervous System - 53%, Pancreas - 47%
86	LG:7698190.26:2002JAN18	widely distributed
87	LG:7763560.12:2002JAN18	Sense Organs - 10%
88	LG:7763587.20:2002JAN18	Sense Organs - 23%, Musculoskeletal System - 12%
89	LG:899263.10:2002JAN18	Female Genitalia - 16%, Nervous System - 16%, Embryonic Structures - 14%, Exocrine Glands - 14%, Liver 14%
90	LG:977837.31:2002JAN18	Liver - 41%, Respiratory System - 29%, Unclassified/Mixed - 29%
91	LG:978560.13:2002JAN18	Germ Cells - 11%, Embryonic Structures - 11%
92	LG:979390.2:2002JAN18	Pancreas - 25%, Connective Tissue - 19%, Liver - 19%
93	LG:983019.1:2002JAN18	Embryonic Structures - 37%, Germ Cells - 29%, Unclassified/Mixed - 11%
94	LG:997202.7:2002JAN18	Skin - 11%, Exocrine Glands - 10%
95	LG:998756.3:2002JAN18	Germ Cells - 20%

TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
96	LG:103460.28:2002JAN18	Germ Cells - 10%
97	LG:1501505.19:2002JAN18	Musculoskeletal System - 50%, Male Genitalia - 33%, Digestive System - 17%
98	LG:233444.9:2002JAN18	Sense Organs - 14%, Urinary Tract - 12%
99	LG:234824.7:2002JAN18	Germ Cells - 21%, Sense Organs - 18%
100	LG:235708.23:2002JAN18	Digestive System - 25%, Liver - 22%, Male Genitalia - 16%
101	LG:236649.14:2002JAN18	Germ Cells - 15%, Musculoskeletal System - 10%
102	LG:332474.7:2002JAN18	Urinary Tract - 56%, Nervous System - 25%, Female Genitalia - 13%
103	LG:335727.8:2002JAN18	Endocrine System - 19%, Cardiovascular System - 18%, Musculoskeletal System - 18%
104	LG:481983.1:2002JAN18	Germ Cells - 12%

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
105	2	168	536	1039	g2827474	1.00E-89	predicted protein dJ257A7.2
105	2	168	536	1039	g15485622	2.00E-51	Q9H4T4 like
105	2	168	536	1039	g10241527	2.00E-51	dJ899C14.1 (novel protein similar to KIAA0680)
106	3	224	3	674	g6599307	1.00E-98	LIM domains containing protein 1
106	3	224	3	674	g12836264	2.00E-98	LIM domains containing 1~data source:MGD, source key:MGI:1352502, evidence:ISS~putative
106	3	224	3	674	g6599070	2.00E-96	LIM domains containing protein 1
107	2	173	614	1132	g24416557	1.00E-87	Similar to amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 7
107	2	173	614	1132	g15823642	1.00E-87	ALS2CR7
107	2	173	614	1132	g4240157	6.00E-51	KIAA0834 protein
108	3	168	870	1373	g20072170	3.00E-20	Unknown (protein for MGC:27348)
108	3	168	870	1373	g2231145	2.00E-15	putative
108	3	168	870	1373	g6522712	1.00E-08	dJ688G8.1 (Similar to ribosomal protein S2 (RPS2))
109	2	187	206	766	g21750807	7.00E-91	unnamed protein product
109	2	187	206	766	g10439850	4.00E-31	unnamed protein product
109	2	187	206	766	g18916783	2.00E-23	KIAA1956 protein
110	2	73	452	670	g930123	4.00E-10	zinc finger protein (583 AA)
110	2	73	452	670	g21758286	5.00E-10	unnamed protein product
110	2	73	452	670	g22760554	8.00E-10	unnamed protein product
111	2	182	59	604	g21739498	2.00E-77	hypothetical protein
111	2	182	59	604	g23273014	2.00E-76	hypothetical protein FLJ37933
111	2	182	59	604	g21754469	4.00E-76	unnamed protein product
112	1	108	133	456	g21754722	2.00E-22	unnamed protein product
112	1	108	133	456	g15080547	2.00E-17	Unknown (protein for MGC:21259)
112	1	108	133	456	g1049301	2.00E-17	KRAB zinc finger protein; Method: conceptual translation supplied by
113	1	240	1	720	g22760908	2.00E-40	unnamed protein product
113	1	240	1	720	g13623633	5.00E-18	Unknown (protein for MGC:13105)
113	1	240	1	720	g16551840	8.00E-16	unnamed protein product
114	2	319	1367	2323	g6808105	1.00E-79	hypothetical protein
114	2	319	1367	2323	g21739797	2.00E-79	hypothetical protein
114	2	319	1367	2323	g19353175	3.00E-79	Unknown (protein for MGC:28436)

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
115	2	263	2	790	g19483967	1.00E-110	RIKEN cDNA 0610009A07 gene
115	2	263	2	790	g12832288	1.00E-110	data source:SPTR, source key:O75989, evidence:ISS~homolog to DJ422F24.1 (PUTATIVE NOVEL PROTEIN SIMILAR TO C. ELEGANS C02C2.5) (FRAGMENT)~putative
115	2	263	2	790	g3757719	2.00E-87	dJ422F24.1 (PUTATIVE novel protein similar to C. elegans C02C2.5)
116	3	449	3	1349	g12839186	0.00	data source:SPTR, source key:Q9VS60, evidence:ISS~putative~related to CG8576 PROTEIN
116	3	449	3	1349	g16553765	0.00	unnamed protein product
116	3	449	3	1349	g23094020	1.00E-108	CG32380-PA
117	1	601	1	1803	g5689563	0.00	KIAA1113 protein
117	1	601	1	1803	g12407441	0.00	tripartite motif protein TRIM33 alpha
117	1	601	1	1803	g5834582	0.00	rfg7 protein
118	2	170	17	526	g16041781	6.00E-85	Similar to RIKEN cDNA 0710001C05 gene
118	2	170	17	526	g23273089	4.00E-82	Unknown (protein for MGC:43081)
118	2	170	17	526	g12833285	3.00E-65	HesB-like domain containing protein~data source:Pfam, source key:PF01521, evidence:ISS~putative
119	3	106	456	773	g9294743	8.00E-37	MAGOH isoform
119	3	106	456	773	g7022229	8.00E-37	unnamed protein product
119	3	106	456	773	g4894380	8.00E-37	Mago homolog
120	2	334	95	1096	g14165480	1.00E-178	Unknown (protein for MGC:1214)
120	2	334	95	1096	g12053195	1.00E-178	hypothetical protein
120	2	334	95	1096	g5305706	1.00E-177	cytoplasmic phosphoprotein PACSIN2
121	2	109	11	337	g17381941	2.00E-43	unnamed protein product
121	2	109	11	337	g999454	7.00E-30	TX protease precursor
121	2	109	11	337	g903934	7.00E-30	cysteine protease
122	1	519	1	1557	g23342615	0.00	unnamed protein product
122	1	519	1	1557	g21899842	0.00	unnamed protein product
122	1	519	1	1557	g21886479	0.00	unnamed protein product
123	3	132	3	398	g21336362	3.00E-24	unnamed protein product
123	3	132	3	398	g21757193	5.00E-22	unnamed protein product
123	3	132	3	398	g7023216	4.00E-17	unnamed protein product
124	2	524	290	1861	g21618499	0.00	Similar to hypothetical protein FLJ20079

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
124	2	524	290	1861	g7019945	1.00E-179	unnamed protein product
124	2	524	290	1861	g22760462	1.00E-165	unnamed protein product
125	1	309	685	1611	g3540177	1.00E-109	F23269_2
125	1	309	685	1611	g5080758	1.00E-108	BC331191_1
125	1	309	685	1611	g12855931	5.00E-63	data source:SPTR, source key:P16374, evidence:ISS~putative~similar to ZINC FINGER PROTEIN 60 (ZFP-60) (ZINC FINGER PROTEIN MFG-3)
126	2	339	1979	2995	g10047329	1.00E-178	KIAA1626 protein
126	2	339	1979	2995	g18256873	1.00E-161	Unknown (protein for IMAGE:4016433)
126	2	339	1979	2995	g7022610	1.00E-151	unnamed protein product
127	2	163	2	490	g12842823	2.00E-38	data source:SPTR, source key:P02403, evidence:ISS~homolog to 60S RIBOSOMAL PROTEIN L37 (G1.16)~putative
127	2	163	2	490	g57121	4.00E-38	ribosomal protein L37
127	2	163	2	490	g461232	4.00E-38	ribosomal protein L37
128	1	352	259	1314	g16552019	1.00E-109	unnamed protein product
128	1	352	259	1314	g12844321	1.00E-96	data source:SPTR, source key:Q9ER30, evidence:ISS~homolog to KELCH-RELATED PROTEIN 1 (KEL-LIKE PROTEIN 23) (SARCOSIN)~putative
128	1	352	259	1314	g16306813	8.00E-39	Unknown (protein for MGC:1367)
129	2	138	2	415	g7582193	5.00E-22	dynein light chain 1 protein DLC-1
129	2	138	2	415	g470344	5.00E-22	C. elegans DLC-1 protein (corresponding sequence T26A5.9)
129	2	138	2	415	g4103059	5.00E-22	protein inhibitor of nitric oxide synthase
130	2	608	1148	2971	g7959175	0.00	KIAA1457 protein
130	2	608	1148	2971	g6599224	0.00	hypothetical protein
130	2	608	1148	2971	g12667438	0.00	NIR3
131	1	694	460	2541	g4929551	0.00	CGI-40 protein
131	1	694	460	2541	g23274030	0.00	Similar to CGI-40 protein
131	1	694	460	2541	g22761032	0.00	unnamed protein product
132	3	401	231	1433	g23242933	0.00	Unknown (protein for MGC:46349)
132	3	401	231	1433	g21755437	0.00	unnamed protein product
132	3	401	231	1433	g20515159	3.00E-15	conserved hypothetical protein
133	3	141	474	896	g4929669	2.00E-70	CGI-100 protein
133	3	141	474	896	g16741027	2.00E-70	CGI-100 protein
133	3	141	474	896	g11596068	2.00E-70	dJ976O13.1 (CGI-100 protein)

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
134	2	340	392	1411	g4164365	0.00	dJ73M23.2 (NAD+-dependent succinic semialdehyde dehydrogenase (SSADH, EC 1.2.1.24))
134	2	340	392	1411	g3766467	0.00	NAD+ dependent succinic semialdehyde dehydrogenase
134	2	340	392	1411	g21708023	0.00	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)
135	3	229	312	998	g7959207	3.00E-38	KIAA1473 protein
135	3	229	312	998	g21265141	7.00E-36	Similar to zinc finger protein 91 (HPF7, HTF10)
135	3	229	312	998	g3342002	9.00E-36	hematopoietic cell derived zinc finger protein
136	1	407	1	1221	g2689444	1.00E-141	ZNF134
136	1	407	1	1221	g10440218	1.00E-130	unnamed protein product
136	1	407	1	1221	g16553223	1.00E-128	unnamed protein product
137	2	529	2	1588	g22477301	0.00	Unknown (protein for MGC:46140)
137	2	529	2	1588	g12852385	0.00	CUG triplet repeat, RNA binding protein 1~data source:MGD, source key:MGI:1342295, evidence:ISS~putative
137	2	529	2	1588	g9246973	0.00	RNA-binding protein BRUNOL2
138	1	2245	2254	8988	g9828190	0.00	FLAMINGO 1
138	1	2245	2254	8988	g21929188	0.00	seven transmembrane helix receptor
138	1	2245	2254	8988	g1665821	0.00	Similar to D.melanogaster cadherin-related tumor suppressor
139	1	490	1	1470	g21595468	1.00E-159	Unknown (protein for MGC:40579)
139	1	490	1	1470	g21749150	1.00E-116	unnamed protein product
139	1	490	1	1470	g23095363	6.00E-97	CG1271-PA
140	2	190	2	571	g12843886	1.00E-15	data source:SPTR, source key:P41276, evidence:ISS~homolog to ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 1~putative
140	2	190	2	571	g607028	2.00E-15	putative
140	2	190	2	571	g20147667	2.00E-15	ADP-ribosylation factor-like protein 1
141	2	153	692	1150	g3953593	2.00E-51	Zinc finger protein s11-6
141	2	153	692	1150	g15928468	2.00E-51	Unknown (protein for MGC:25259)
141	2	153	692	1150	g21751975	3.00E-51	unnamed protein product
142	1	608	583	2406	g3327176	0.00	KIAA0681 protein
142	1	608	583	2406	g11323324	0.00	dJ138B7.3.2 (lethal (3) malignant brain tumor (l(3)mbt) protein (Drosophila) homolog (isoform 2) (KIAA0681))
142	1	608	583	2406	g3811111	0.00	l(3)mbt protein homolog

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
143	1	265	646	1440	g21752073	1.00E-148	unnamed protein product
143	1	265	646	1440	g16041142	1.00E-133	hypothetical protein
143	1	265	646	1440	g14017813	1.00E-88	KIAA1798 protein
144	2	687	8	2068	g12024744	0.00	TA p63 alpha
144	2	687	8	2068	g3970717	0.00	KET protein
144	2	687	8	2068	g3695094	0.00	TA*p63 alpha
145	1	478	1	1434	g15620895	0.00	KIAA1918 protein
145	1	478	1	1434	g971459	0.00	UDP-GalNAc:polypeptide N-acetylgalactosaminyl transferase
145	1	478	1	1434	g304259	0.00	UDP-GalNAc:polypeptide, N-acetylgalactosaminyltransferase
146	1	946	274	3111	g10047283	0.00	KIAA1604 protein
146	1	946	274	3111	g10439972	0.00	unnamed protein product
146	1	946	274	3111	g10438214	0.00	unnamed protein product
147	3	318	3	956	g6572215	1.00E-170	dJ37E16.5 (novel protein similar to nitrophenylphosphatases from various organisms)
147	3	318	3	956	g12653107	1.00E-170	hypothetical protein dJ37E16.5
147	3	318	3	956	g14602499	5.00E-99	Similar to hypothetical protein dJ37E16.5
148	3	1632	3	4898	g12083896	0.00	polybromo-1
148	3	1632	3	4898	g12083875	0.00	polybromo-1
148	3	1632	3	4898	g16607752	0.00	unnamed protein product
149	2	736	2	2209	g12836469	0.00	data source:SPTR, source key:Q9HCJ3, evidence:ISS~homolog to KIAA1579 PROTEIN (FRAGMENT)~putative
149	2	736	2	2209	g22902182	0.00	Unknown (protein for IMAGE:5113697)
149	2	736	2	2209	g22766819	0.00	Unknown (protein for MGC:46327)
150	1	323	157	1125	g16588681	1.00E-161	anion transporter/exchanger-9
150	1	323	157	1125	g15341556	1.00E-161	putative anion transporter
150	1	323	157	1125	g14787223	2.00E-29	prestin
151	1	628	1	1884	g7959287	0.00	KIAA1513 protein
151	1	628	1	1884	g20146520	1.00E-101	SLTP003
151	1	628	1	1884	g14670188	3.00E-27	Hypothetical protein W02H5.4
152	3	183	324	872	g21758740	3.00E-92	unnamed protein product
152	3	183	324	872	g20073240	3.00E-92	similar to putative
152	3	183	324	872	g15795887	3.00E-92	unnamed protein product

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
153	1	338	499	1512	g6329959	1.00E-132	KIAA1142 protein
153	1	338	499	1512	g4164385	1.00E-132	PAK4 protein
153	1	338	499	1512	g4101587	1.00E-132	serine/threonine kinase
154	1	191	25	597	g22760075	1.00E-103	unnamed protein product
154	1	191	25	597	g15209772	3.00E-99	unnamed protein product
154	1	191	25	597	g20377682	5.00E-92	P26 protein
155	3	317	3	953	g21542541	1.00E-119	Similar to HTPAP protein
155	3	317	3	953	g13182757	3.00E-85	HTPAP
155	3	317	3	953	g12844263	3.00E-58	data source:SPTR, source key:Q9VND5, evidence:ISS~putative~related to CG12746 PROTEIN
156	2	617	8	1858	g23273603	0.00	Unknown (protein for MGC:37640)
156	2	617	8	1858	g10041649	0.00	unnamed protein product
156	2	617	8	1858	g23271317	0.00	Unknown (protein for MGC:33943)
157	3	371	1197	2309	g20988140	0.00	E74-like factor 1 (ets domain transcription factor)
157	3	371	1197	2309	g15010800	0.00	Ets-family transcription factor ELF1
157	3	371	1197	2309	g11995007	0.00	transcription factor Elf-1
158	2	871	989	3601	g20372683	0.00	euchromatic histone methyltransferase 1
158	2	871	989	3601	g10434623	0.00	unnamed protein product
158	2	871	989	3601	g20522002	0.00	KIAA1876 protein
159	2	157	152	622	g18490501	1.00E-56	RIKEN cDNA 2010002A20 gene
159	2	157	152	622	g12843712	1.00E-56	Immunoglobulin domain containing protein~data source:Pfam, source key:PF00047, evidence:ISS~putative
159	2	157	152	622	g12841961	1.00E-50	Immunoglobulin domain containing protein~data source:Pfam, source key:PF00047, evidence:ISS~putative
160	1	280	10	849	g23451450	1.00E-122	ATP-binding cassette sub-family A member 9
160	1	280	10	849	g23451407	1.00E-122	ATP-binding cassette sub-family A member 9
160	1	280	10	849	g17223624	1.00E-121	ATP-binding cassette A9
161	1	149	559	1005	g18088580	1.00E-80	Unknown (protein for MGC:23949)
161	1	149	559	1005	g12860781	1.00E-30	claudin 14~data source:MGD, source key:MGI:1860425, evidence:ISS~putative
161	1	149	559	1005	g13452508	1.00E-30	claudin 14
162	3	281	270	1112	g16549414	1.00E-155	unnamed protein product

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
162	3	281	270	1112	g13938457	1.00E-155	Unknown (protein for MGC:16175)
162	3	281	270	1112	g13436338	1.00E-77	Unknown (protein for IMAGE:3625550)
163	3	703	312	2420	g13811938	0.00	dJ1056H1.2.1 (novel protein similar to mitogen inducible protein MIG-2 (isoform 1))
163	3	703	312	2420	g23273527	0.00	Unknown (protein for MGC:46404)
163	3	703	312	2420	g16878257	0.00	Unknown (protein for MGC:29726)
164	1	128	439	822	g24059753	5.00E-64	hypothetical protein
164	1	128	439	822	g12856090	9.00E-62	data source:SPTR, source key:Q9Z2B2, evidence:ISS~putative~similar to BRAIN MITOCHONDRIAL CARRIER PROTEIN-1 (BMCP-1)
164	1	128	439	822	g12854104	9.00E-62	data source:SPTR, source key:Q9Z2B2, evidence:ISS~putative~similar to BRAIN MITOCHONDRIAL CARRIER PROTEIN-1 (BMCP-1)
165	2	1250	2	3751	g21756799	0.00	unnamed protein product
165	2	1250	2	3751	g13938013	0.00	Similar to RIKEN cDNA 2610509G12 gene
165	2	1250	2	3751	g6650822	0.00	PRO2000
166	1	705	1	2115	g13365895	0.00	hypothetical protein
166	1	705	1	2115	g21749428	0.00	unnamed protein product
166	1	705	1	2115	g1842216	8.00E-17	Zfp64
167	3	630	3	1892	g717056	0.00	reduced folate carrier protein
167	3	630	3	1892	g2209135	0.00	folate carrier
167	3	630	3	1892	g2967654	0.00	reduced folate carrier
168	3	389	132	1298	g12832845	1.00E-161	Domain of unknown function DUF36 containing protein~data source:Pfam, source key:PF01795, evidence:ISS~putative
168	3	389	132	1298	g21749636	1.00E-136	unnamed protein product
168	3	389	132	1298	g21410962	1.00E-70	Unknown (protein for MGC:32708)
169	2	381	83	1225	g5114351	1.00E-165	RING finger protein terf
169	2	381	83	1225	g21707131	1.00E-165	tripartite motif-containing 17
169	2	381	83	1225	g5114353	1.00E-118	RING finger protein terf
170	3	659	3	1979	g14017797	0.00	KIAA1790 protein
170	3	659	3	1979	g13529311	1.00E-126	Similar to hypothetical protein FLJ23119
170	3	659	3	1979	g10439701	1.00E-109	unnamed protein product
171	2	219	1253	1909	g8096557	1.00E-84	PBX1B
171	2	219	1253	1909	g8096555	1.00E-84	PBX1A

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
171	2	219	1253	1909	g456109	1.00E-84	homeobox protein
172	2	438	2	1315	g22859174	0.00	hypothetical protein
172	2	438	2	1315	g12845866	1.00E-124	Zinc finger,. C3HC4 type (RING finger) containing protein~data source:Pfam, source key:PF00097, evidence:ISS~putative
172	2	438	2	1315	g13477235	1.00E-82	Similar to RIKEN cDNA 0610037N03 gene
173	1	106	1	318	g15741221	1.00E-17	gene overexpressed in astrocytoma
173	1	106	1	318	g458726	2.00E-13	estrogen responsive finger protein (efp)
173	1	106	1	318	g16877339	2.00E-13	zinc finger protein 147 (estrogen-responsive finger protein)
174	2	357	2	1072	g4239984	1.00E-143	insulin receptor substrate protein of 53 kDa (a shorter form)
174	2	357	2	1072	g4239982	1.00E-143	insulin receptor substrate protein of 53 kDa (a longer form)
174	2	357	2	1072	g4126477	1.00E-143	BAP2-beta protein
175	3	266	546	1343	g3327220	1.00E-123	KIAA0703 protein
175	3	266	546	1343	g19550878	1.00E-103	putative secretory pathway Ca-ATPase SPCA2
175	3	266	546	1343	g20072000	2.00E-99	Unknown (protein for IMAGE:4984604)
176	3	470	255	1664	g16033591	0.00	SH2 domain-containing phosphatase anchor protein 2b
176	3	470	255	1664	g18092655	0.00	immunoglobulin superfamily receptor translocation associated protein 3
176	3	470	255	1664	g16033588	0.00	SH2 domain-containing phosphatase anchor protein 2a
177	3	938	3	2816	g22597198	0.00	enaptin
177	3	938	3	2816	g24417709	0.00	nesprin-1
177	3	938	3	2816	g22597200	0.00	enaptin165 short isoform
178	3	928	21	2804	g13365845	0.00	hypothetical protein
178	3	928	21	2804	g4589506	0.00	KIAA0931 protein
178	3	928	21	2804	g20521103	0.00	KIAA0606 protein
179	2	304	2	913	g14198272	1.00E-139	Unknown (protein for MGC:5352)
179	2	304	2	913	g12848731	1.00E-123	data source:SPTR, source key:O46084, evidence:ISS~putative~related to EG:63B12.4 PROTEIN
179	2	304	2	913	g23820820	1.00E-63	Hypothetical protein R07G3.5
180	3	320	207	1166	g13185169	1.00E-170	unnamed protein product
180	3	320	207	1166	g17390445	1.00E-167	g1-related zinc finger protein
180	3	320	207	1166	g6175860	1.00E-167	g1-related zinc finger protein
181	2	358	218	1291	g21755898	0.00	unnamed protein product
181	2	358	218	1291	g18204012	0.00	Similar to RIKEN cDNA B830026H24 gene

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
181	2	358	218	1291	g12861800	0.00	data source:SPTR, source key:P97584, evidence:ISS~homolog to NADP-DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE (EC 1.1.1.-) (DITHIOLETHIONE-INDUCIBLE GENE-1)~putative
182	1	438	154	1467	g20521722	0.00	KIAA1004 protein
182	1	438	154	1467	g10440530	0.00	FLJ00115 protein
182	1	438	154	1467	g5917730	3.00E-92	F-box protein Lilina
183	1	246	280	1017	g21739365	1.00E-129	hypothetical protein
183	1	246	280	1017	g14424793	1.00E-127	Unknown (protein for MGC:15165)
183	1	246	280	1017	g4929679	1.00E-126	CGI-105 protein
184	3	266	354	1151	g4210363	1.00E-131	FUS gycline rich protein
184	3	266	354	1151	g386157	1.00E-131	TLS
184	3	266	354	1151	g3582784	1.00E-131	FUS/TLS protein
185	3	539	3	1619	g12275901	0.00	tripartite motif protein TRIM19 zeta
185	3	539	3	1619	g12275899	0.00	tripartite motif protein TRIM19 epsilon
185	3	539	3	1619	g12275897	0.00	tripartite motif protein TRIM19 delta
186	1	242	1	726	g21752509	1.00E-151	unnamed protein product
186	1	242	1	726	g22761208	9.00E-90	unnamed protein product
186	1	242	1	726	g5262557	1.00E-88	hypothetical protein
187	2	194	938	1519	g22760718	1.00E-116	unnamed protein product
187	2	194	938	1519	g21739830	1.00E-116	hypothetical protein
187	2	194	938	1519	g21618492	1.00E-116	Unknown (protein for MGC:45380)
188	1	149	145	591	g21336098	1.00E-84	unnamed protein product
188	1	149	145	591	g7959207	3.00E-26	KIAA1473 protein
188	1	149	145	591	g498736	4.00E-26	zinc finger protein
189	3	268	756	1559	g12314164	1.00E-151	bA526D8.2 (novel protein similar to KIAA1074)
189	3	268	756	1559	g12314195	1.00E-134	bA255A11.3 (novel protein similar to KIAA1074)
189	3	268	756	1559	g12053099	3.00E-96	hypothetical protein
190	3	1304	3	3914	g5931959	0.00	acinusL
190	3	1304	3	3914	g3327154	0.00	KIAA0670 protein
190	3	1304	3	3914	g9622185	0.00	acinusL protein
192	2	837	41	2551	g15917538	0.00	NG36/G9a
192	2	837	41	2551	g21832045	0.00	G9a short

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
192	2	837	41	2551	g21832049	0.00	G9a long
193	2	445	35	1369	g12857369	1.00E-123	data source:SPTR, source key:Q9UII4, evidence:ISS~homolog to CYCLIN-E BINDING PROTEIN 1~putative
193	2	445	35	1369	g12846911	1.00E-113	data source:SPTR, source key:Q9UII4, evidence:ISS~homolog to CYCLIN-E BINDING PROTEIN 1~putative
193	2	445	35	1369	g21750989	9.00E-97	unnamed protein product
194	1	139	532	948	g22760684	3.00E-50	unnamed protein product
194	1	139	532	948	g12858264	7.00E-48	data source:SPTR, source key:P70193, evidence:ISS~putative~similar to MEMBRANE GLYCOPROTEIN
194	1	139	532	948	g1545807	3.00E-31	membrane glycoprotein
195	2	650	287	2236	g10047251	0.00	KIAA1588 protein
195	2	650	287	2236	g16797866	0.00	ZNF317-4 protein
195	2	650	287	2236	g16797860	0.00	ZNF317-2 protein
196	1	157	1	471	g14250235	2.00E-17	RIKEN cDNA 4633401C23 gene
196	1	157	1	471	g12852573	2.00E-17	Zinc finger domain containing protein~data source:InterPro, source key:IPR000822, evidence:ISS~putative
196	1	157	1	471	g340446	3.00E-17	zinc finger protein 7 (ZFP7)
197	2	431	2	1294	g5738952	0.00	hTbr2
197	2	431	2	1294	g9711283	0.00	Tbr2
197	2	431	2	1294	g5738950	0.00	Tbr2
198	2	975	158	3082	g6959306	0.00	BOG25
198	2	975	158	3082	g21961541	0.00	expressed sequence AI594717
198	2	975	158	3082	g15126721	0.00	Similar to SH3-domain binding protein 4
199	1	484	1	1452	g24181967	0.00	NEW1 domain containing protein
199	1	484	1	1452	g24181969	0.00	NEW1 domain containing protein isoform
199	1	484	1	1452	g24181965	0.00	NEW1 domain containing protein
200	2	275	518	1342	g7022363	1.00E-160	unnamed protein product
200	2	275	518	1342	g4325215	1.00E-160	single-strand selective monofunctional uracil DNA glycosylase
200	2	275	518	1342	g19339024	1.00E-160	SMUG1
201	1	245	1	735	g23273536	3.00E-97	Unknown (protein for MGC:46523)
201	1	245	1	735	g22761212	3.00E-97	unnamed protein product
201	1	245	1	735	g22207737	3.00E-97	unnamed protein product

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
202	2	247	527	1267	g7020081	1.00E-134	unnamed protein product
202	2	247	527	1267	g7023136	1.00E-134	unnamed protein product
202	2	247	527	1267	g13278516	1.00E-101	Similar to hypothetical protein FLJ10846
203	2	749	1034	3280	g4239895	0.00	MASL1
203	2	749	1034	3280	g15559745	0.00	Similar to MFH-amplified sequences with leucine-rich tandem repeats 1
203	2	749	1034	3280	g19916243	3.00E-14	hypothetical protein
204	1	330	910	1899	g21756391	9.00E-27	unnamed protein product
205	1	301	133	1035	g20067239	1.00E-118	putative regulation protein GS3
205	1	301	133	1035	g12859941	3.00E-56	evidence:NAS~hypothetical protein~putative
205	1	301	133	1035	g5052516	7.00E-25	BcDNA.GH03108
206	1	213	1	639	g21739500	1.00E-08	hypothetical protein
206	1	213	1	639	g456269	3.00E-05	zinc finger protein 30
206	1	213	1	639	g12851705	3.00E-05	data source:MGD, source key:MGI:99178, evidence:ISS~putative~zinc finger protein 30
207	2	322	2	967	g15559324	1.00E-180	Unknown (protein for IMAGE:4309224)
207	2	322	2	967	g16551666	1.00E-173	unnamed protein product
207	2	322	2	967	g21739611	1.00E-109	hypothetical protein
208	3	238	381	1094	g21410798	1.00E-80	Unknown (protein for IMAGE:4396549)
208	3	238	381	1094	g19526448	2.00E-69	TRH4
208	3	238	381	1094	g21618502	4.00E-68	Similar to RIKEN cDNA 2310081H14 gene

TABLE 8

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25:3389-3402.	ESTs: Probability value= 1.0E-8 or less; Full Length sequences: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises as least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad Sci. USA 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183:63-98; and Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489.	ESTs: fasta E value=1.06E-6; Assembled ESTs: fasta Identity= 95% or greater and Match length=200 bases or greater; fastx E value=1.0E-8 or less; Full Length sequences: fastx score=100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS, PRINTS, DOMO, PRODOM, and PFAM databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff (1991) Nucleic Acids Res. 19:6565-6572; Henikoff, J.G. and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37:417-424.	Probability value= 1.0E-3 or less
HMMER	An algorithm for searching a query sequence against hidden Markov model (HMM)-based databases of protein family consensus sequences, such as PFAM.	Krogh, A. et al. (1994) J. Mol. Biol. 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) Nucleic Acids Res. 26:320-322; Durbin, R. et al. (1998) Our World View, in a Nutshell, Cambridge Univ. Press, pp. 1-350.	PFAM hits: Probability value= 1.0E-3 or less; Signal peptide hits: Score= 0 or greater

TABLE 8

Program	Description	Reference	Parameter Threshold
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, M. et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221.	Normalized quality score≥GCG-specified "HIGH" value for that particular Prosite motif. Generally, score=1.4-2.1.
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M.S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies.	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12:431-439.	Score=3.5 or greater
TMAP	A program that uses weight matrices to delineate transmembrane segments on protein sequences and determine orientation.	Persson, B. and P. Argos (1994) J. Mol. Biol. 237:182-192; Persson, B. and P. Argos (1996) Protein Sci. 5:363-371.	
TMHMMER	A program that uses a hidden Markov model (HMM) to delineate transmembrane segments on protein sequences and determine orientation.	Sonnhammer, E.L. et al. (1998) Proc. Sixth Intl. Conf. On Intelligent Systems for Mol. Biol., Glasgow et al., eds., The Am. Assoc. for Artificial Intelligence (AAAI) Press, Menlo Park, CA, and MIT Press, Cambridge, MA, pp. 175-182.	

TABLE 8

Program	Description	Reference	Parameter Threshold
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

CLAIMS

What is claimed is:

1. An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:

a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104,

b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104,

c) a polynucleotide sequence complementary to a),

d) a polynucleotide sequence complementary to b), and

e) an RNA equivalent of a) through d).

2. An isolated polynucleotide of claim 1, comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-104.

3. An isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide of claim 1.

4. A composition for the detection of expression of disease detection and treatment molecule polynucleotides comprising at least one of the polynucleotides of claim 1 and a detectable label.

5. A method for detecting a target polynucleotide in a sample, said target polynucleotide comprising a sequence of a polynucleotide of claim 1, the method comprising:

a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and

b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

6. A method for detecting a target polynucleotide in a sample, said target polynucleotide comprising a sequence of a polynucleotide of claim 1, the method comprising:

a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and

b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

7. A method of claim 5, wherein the probe comprises at least 30 contiguous nucleotides.

8. A method of claim 5, wherein the probe comprises at least 60 contiguous nucleotides.

9. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 1.

10. A cell transformed with a recombinant polynucleotide of claim 9.

11. A transgenic organism comprising a recombinant polynucleotide of claim 9.

12. A method for producing a disease detection and treatment molecule polypeptide, the method comprising:

a) culturing a cell under conditions suitable for expression of the disease detection and treatment molecule polypeptide, wherein said cell is transformed with a recombinant polynucleotide of claim 9, and

b) recovering the disease detection and treatment molecule polypeptide so expressed.

13. A purified disease detection and treatment molecule polypeptide (MDDT) encoded by at least one of the polynucleotides of claim 2.

14. An isolated antibody which specifically binds to a disease detection and treatment molecule polypeptide of claim 13.

15. A method of identifying a test compound which specifically binds to the disease detection and treatment molecule polypeptide of claim 13, the method comprising the steps of:

a) providing a test compound;

b) combining the disease detection and treatment molecule polypeptide with the test compound for a sufficient time and under suitable conditions for binding; and

c) detecting binding of the disease detection and treatment molecule polypeptide to the test compound, thereby identifying the test compound which specifically binds the disease detection and treatment molecule polypeptide.

16. A microarray wherein at least one element of the microarray is a polynucleotide of claim 3.

17. A method for generating a transcript image of a sample which contains polynucleotides, the method comprising the steps of:

a) labeling the polynucleotides of the sample,

b) contacting the elements of the microarray of claim 16 with the labeled polynucleotides of the sample under conditions suitable for the formation of a hybridization complex, and

c) quantifying the expression of the polynucleotides in the sample.

18. A method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a polynucleotide sequence of claim 1, the method comprising:

a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,

b) detecting altered expression of the target polynucleotide, and

c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

19. A method for assessing toxicity of a test compound, said method comprising:

a) treating a biological sample containing nucleic acids with the test compound;

b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 1 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 1 or fragment thereof;

c) quantifying the amount of hybridization complex; and

d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

20. An array comprising different nucleotide molecules affixed in distinct physical locations on a solid substrate, wherein at least one of said nucleotide molecules comprises a first

oligonucleotide or polynucleotide sequence specifically hybridizable with at least 30 contiguous nucleotides of a target polynucleotide, said target polynucleotide having a sequence of claim 1.

21. An array of claim 20, wherein said first oligonucleotide or polynucleotide sequence is completely complementary to at least 30 contiguous nucleotides of said target polynucleotide.

22. An array of claim 20, wherein said first oligonucleotide or polynucleotide sequence is completely complementary to at least 60 contiguous nucleotides of said target polynucleotide

23. An array of claim 20, which is a microarray.

24. An array of claim 20, further comprising said target polynucleotide hybridized to said first oligonucleotide or polynucleotide.

25. An array of claim 20, wherein a linker joins at least one of said nucleotide molecules to said solid substrate.

26. An array of claim 20, wherein each distinct physical location on the substrate contains multiple nucleotide molecules having the same sequence, and each distinct physical location on the substrate contains nucleotide molecules having a sequence which differs from the sequence of nucleotide molecules at another physical location on the substrate.

27. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

a) an amino acid sequence selected from the group consisting of SEQ ID NO:105-208,

b) a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:105-208,

c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:105-208, and

d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:105-208.

28. An isolated polypeptide of claim 27, comprising a polypeptide sequence selected from the group consisting of SEQ ID NO:105-208.

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<213> Homo sapiens

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<213> Homo sapiens

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<213> Homo sapiens

<220>

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<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

<220>
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<223> Incyte ID No: LG:234430.7:2002JAN18

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<212> DNA
<213> Homo sapiens

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<211> 1543
<212> DNA
<213> Homo sapiens

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<210> 57
<211> 1007
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:280014.1:2002JAN18

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<212> DNA
<213> Homo sapiens

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<213> Homo sapiens

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<213> Homo sapiens

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<400> 82

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<213> Homo sapiens

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<220>
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<223> a, t, c, g, or other

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<213> Homo sapiens

<220>
<221> misc_feature

<223> Incyte ID No: LG:7690373.1:2002JAN18

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<212> DNA
<213> Homo sapiens

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<212> DNA
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<220>
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<212> DNA
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taaataataa tagccctgag atgtttctaa catttaaata agaaaaaaat caaatcgaag 4980
tcagcctgct ggaaaagtga tcacatggca gttgcagtaa cttgtatgga aagagaaaat 5040
gcaatgagcc cagttactgc acttgccact accatgctgt ccatggaagg aataatcagc 5100
agttcagttg tcacaagccg cccttgaaga aaacgcagca aaatatttta aaatgaagat 5160
attgcagtcc ccagagccag tgaaggtttc ttttggtaaa atgaaattgt gccattgtca 5220
aagtaccccg tagtgatgag cactgactgg ttcactggcc acattttagt tcttcataat 5280
aataggccac aaaagggctc tgtggtttgc ctccatgtgc actggcccct ccccacccct 5340
agggggcact cagtagctgc tgagaaggcc tgtccacgag gctgttggaa cccctccaat 5400
aaatacttag aggtagtgta tctgatgctt gttttcgtgg agaaaattgt attggagaac 5460
ttaaaacatc acgaatattt ttaataggat ccgcagacac ccaaaggaga agcttggtct 5520
tttccaggta tttccaactt gagttcaacc caaagccttt gaaaggaatg cattaccaca 5580
tgaccacatg ctgagacccc atggggtcta acacggacc taagaaagtc tctgcagcca 5640
gatagtacat ggtgtctcca caaaactagg cattctggag attgcccaga aagggatgtg 5700

aggggaccgt taagatctgt cttgcttatc tcatgcactc acattccttc agcctcctgg 5760
agttcctgat aaaaggaagc cagggtgttg acatttttta gctattgatt tcccaatagc 5820
ttgtggatca gttgtacacc cacacttcct tctctgccta attccgtttt tctggaaaaa 5880
gtagtatgcc catgtatgtg tgtttttctt aacacaggtc catgaaagtt tggcttcctg 5940
gtttgatgtc tgttgcgtgg cctggaaacc agggagcagc aactattgag atggtttctg 6000
tgttcagtga aaaattctat ttcattgaga caatttttc tttatccaca gtaattttt 6060
gacactgtca tcatgaaact accttagga aaataagatt acctgcaaaa aaaaaaaaga 6120
aatgagttat ggaataggaa cagttatgtg atgattctga aactttaact tagagcttca 6180
ttactttaag aatggaaaac aacctctgag tttgatttcc caaagtttca taaagcccct 6240
aagctcatga ttttcatcaa ctctttgccc acatagtcat ttacctccac agccgtttgt 6300
tgtcatagaa ggggtggtgg tgtttggatt tgattttttt caacttgcag tgagaaatag 6360
gataggtgac aaaaccttac ttgttttctt aagacaattc agtgcttgag catctctgtc 6420
agaaatggaa tgaaatactg ttagccaatt agaattattt tatgtattgt tattgtgttt 6480
tgctgatttt tatatgaaaa tataattatt cattcttgat ctctggaagc aatcattatt 6540
atgaggatca ttttactttg gaaacacttt cataataaag ataagtatta agagtgcagt 6600
gtaagtgccc tttactgtaa atgctaacca gctcgtgtgg gtaaaacatc acatctcacc 6660
tgatgaggtt aataaaggct cacatcatcc cagtagattg ttacaagcct cgtcaactcc 6720
cagtatcatt gtgatcattg agaaagtaat gttacgttaa cttggataga ctgtagtatc 6780
tctttgaaaa ttaagattaa aacctcaatg ctaaa 6815

<210> 105
<211> 168
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:1447398.9.orf2:2002JAN18

<400> 105
Gly Gly Gly Gly Gly Glu Ser Gln Ser Phe Arg Ala Gln Asp Gly
1 5 10 15
Thr Arg Thr Pro Ala Thr Asp Cys Leu Met Tyr Leu Gln Gly Pro
20 25 30
Arg Lys Leu Met Thr Gln Gly Gly Tyr Asp Met Val Gln Lys Leu
35 40 45
Phe Leu Asp Phe Phe Arg Arg Arg Leu Ser Gln Arg Pro Thr Ala
50 55 60
Glu Glu Leu Glu Gln Arg Asn Ile Leu Lys Pro Arg Asn Glu Gln
65 70 75
Glu Glu Gln Glu Glu Lys Arg Glu Ile Lys Arg Arg Leu Thr Arg
80 85 90
Lys Leu Ser Gln Arg Pro Thr Val Glu Glu Leu Arg Glu Arg Lys
95 100 105
Ile Leu Ile Arg Phe Ser Asp Tyr Val Glu Val Ala Asp Ala Gln
110 115 120
Asp Tyr Asp Arg Arg Ala Asp Lys Pro Trp Thr Arg Leu Thr Ala
125 130 135
Ala Asp Lys Ala Ala Ile Arg Lys Glu Leu Asn Glu Phe Lys Ser
140 145 150
Thr Glu Met Glu Val His Glu Leu Ser Arg His Leu Thr Arg Phe
155 160 165
His Arg Pro

<210> 106
<211> 224
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:201488.3.orf3:2002JAN18

<400> 106
Arg Glu Leu Glu Arg Ala Leu Glu Ala Arg Thr Ala Arg Asp Tyr
1 5 10 15
Phe Gly Ile Cys Ile Lys Cys Gly Leu Gly Ile Tyr Gly Ala Gln
20 25 30
Gln Ala Cys Gln Ala Met Gly Ser Leu Tyr His Thr Asp Cys Phe
35 40 45
Thr Cys Asp Ser Cys Gly Arg Arg Leu Arg Gly Lys Ala Phe Tyr
50 55 60
Asn Val Gly Glu Lys Val Tyr Cys Gln Glu Asp Phe Leu Tyr Ser
65 70 75
Gly Phe Gln Gln Thr Ala Asp Lys Cys Ser Val Cys Gly His Leu
80 85 90
Ile Met Glu Met Ile Leu Gln Ala Leu Gly Lys Ser Tyr His Pro
95 100 105
Gly Cys Phe Arg Cys Ser Val Cys Asn Glu Cys Leu Asp Gly Val
110 115 120
Pro Phe Thr Val Asp Val Glu Asn Asn Ile Tyr Cys Val Arg Asp
125 130 135
Tyr His Thr Val Phe Ala Pro Lys Cys Ala Ser Cys Ala Arg Pro
140 145 150
Ile Leu Pro Ala Gln Gly Cys Glu Thr Thr Ile Arg Val Val Ser
155 160 165
Met Asp Arg Asp Tyr His Val Ala Cys Tyr His Cys Glu Asp Cys
170 175 180
Gly Leu Gln Leu Ser Gly Glu Glu Gly Arg Arg Cys Tyr Pro Leu
185 190 195
Ala Gly His Leu Leu Cys Arg Arg Cys His Leu Arg Arg Leu Gln
200 205 210
Pro Gly Pro Leu Pro Ser Pro Thr Val His Val Thr Glu Leu
215 220

<210> 107
<211> 173
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:288410.6.orf2:2002JAN18

<400> 107
Asn Leu Arg Thr Tyr Ser Ser Val Thr Trp Glu Ser Ser Asn Trp
1 5 10 15
Leu Ile Cys Gly Leu Ala Arg Ala Lys Ser Ile Pro Ser Gln Thr
20 25 30
Tyr Ser Ser Glu Val Val Thr Leu Trp Tyr Arg Pro Pro Asp Ala
35 40 45
Leu Leu Gly Ala Thr Glu Tyr Ser Ser Glu Leu Asp Ile Trp Gly
50 55 60
Ala Gly Cys Ile Phe Ile Glu Met Phe Gln Gly Gln Pro Leu Phe
65 70 75
Pro Gly Val Ser Asn Ile Leu Glu Gln Leu Glu Lys Ile Trp Glu
80 85 90
Val Leu Gly Val Pro Thr Glu Asp Thr Trp Pro Gly Val Ser Lys
95 100 105
Leu Pro Asn Tyr Asn Pro Glu Trp Phe Pro Leu Pro Thr Pro Arg
110 115 120
Ser Leu His Val Val Trp Asn Arg Leu Gly Arg Val Pro Glu Ala
125 130 135
Glu Asp Leu Ala Ser Gln Met Leu Lys Gly Phe Pro Arg Asp Arg
140 145 150
Val Ser Ala Gln Glu Ala Leu Val His Asp Tyr Phe Ser Ala Leu

155 160 165
Pro Ser Gln Leu Tyr Gln Thr Ser
170

<210> 108
<211> 168
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:7682817.1.orf3:2002JAN18

<400> 108
Leu Gly Ala Leu Ser Arg Met Arg Phe Glu Asp Tyr Ala Asn Ala
1 5 10 15
Glu Ala His Val His Gln Pro Ala His Gln Val Gln Gly Ile Cys
20 25 30
Cys Leu Gln Gly Leu Glu Arg Ser Arg Leu Val Trp Val Leu Ser
35 40 45
Val Pro Arg Arg Cys Arg Pro Arg Gly His His Ser Gly Gln Ala
50 55 60
Phe His Cys Ser Arg Ala Gln Arg Leu Leu Gly Glu Gln Asp Gln
65 70 75
Gln Ala Pro His His Pro Leu Gln Gly Asp Arg Pro Leu Gln Leu
80 85 90
Cys Ala Cys Ala Pro His Pro Cys Ala Gln Gly His Trp Cys His
95 100 105
Leu Gly Pro Arg Tyr Ser Leu Glu Cys Cys Cys Leu Val Ala Gly
110 115 120
Ile Asp Asp Cys Tyr Thr Ser Ala Arg Ser Cys Thr Ala Thr Leu
125 130 135
Gly Asn Phe Ala Lys Thr Thr Phe Asp Ala Ile Ser Ile Asp Leu
140 145 150
Gln Leu Pro Asp Pro Arg Pro Leu Glu Glu Asp Cys Val His Gln
155 160 165
Val Ser Leu

<210> 109
<211> 187
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:7685059.6.orf2:2002JAN18

<400> 109
Gly Pro Leu Ser Pro Gly Pro Tyr Gln Cys Arg Pro Ser Leu Pro
1 5 10 15
Ala Gln Leu Tyr Pro Gln Ser Leu Met Ala Ala Ala Thr Leu Arg
20 25 30
Thr Pro Thr Gln Gly Thr Val Thr Phe Glu Asp Val Ala Val His
35 40 45
Phe Ser Trp Glu Glu Trp Gly Leu Leu Asp Glu Ala Gln Arg Cys
50 55 60
Leu Tyr Arg Asp Val Met Leu Glu Asn Leu Ala Leu Leu Thr Ser
65 70 75
Leu Asp Val His His Gln Lys Gln His Leu Gly Glu Lys His Phe
80 85 90
Arg Ser Asn Val Gly Arg Ala Leu Phe Val Lys Thr Cys Thr Phe
95 100 105

His Val Ser Gly Glu Pro Ser Thr Cys Arg Glu Val Gly Lys Asp
110 115 120
Phe Leu Ala Lys Leu Gly Phe Leu His Gln Gln Ala Ala His Thr
125 130 135
Gly Glu Gln Ser Asn Ser Lys Ser Asp Val Gly Ala Ile Ser His
140 145 150
Arg Gly Lys Thr His Cys Asn Cys Gly Glu His Thr Lys Ala Phe
155 160 165
Ser Gly Lys His Thr Leu Val Gln Gln Gln Arg Thr Leu Thr Thr
170 175 180
Glu Arg Cys Tyr Ile Arg Ser
185

<210> 110
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:7689671.1.orf2:2002JAN18

<400> 110
Arg Glu Ser Glu Gly Lys Glu Asp Gly Gln Cys Glu Glu Ile Phe
1 5 10 15
Ser Leu Val Pro Asn Gly Ile Val Lys Thr Thr Phe Thr Gly Val
20 25 30
Lys Ser Cys Glu Ser Ser Val Cys Glu Glu Gly Asn Met Asp His
35 40 45
Ser Ser Leu Asn Cys Cys Ile Arg Ala Asp Thr Gly His Lys Ser
50 55 60
Asp Glu Cys Gln Gln His Arg Ser His Ile Ser Ser Val
65 70

<210> 111
<211> 182
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:7689684.1.orf2:2002JAN18

<400> 111
Pro Lys Gln Gly Ile Arg Val Trp Ser Pro Arg His Pro Glu Asn
1 5 10 15
Phe Leu Gly Ile Glu Ser Arg Pro Pro Val Leu Ser Leu Ser Pro
20 25 30
Ile Leu Leu Tyr Thr Cys Glu Met Phe Gln Asp Pro Val Ala Phe
35 40 45
Asp Asp Val Ala Val Asn Phe Thr Gln Glu Glu Trp Ala Leu Leu
50 55 60
Asp Ile Ser Gln Arg Lys Leu Tyr Lys Glu Val Met Leu Glu Thr
65 70 75
Phe Arg Asn Leu Thr Ser Val Gly Lys Ser Trp Lys Asp Gln Asn
80 85 90
Ile Glu Tyr Glu Tyr Gln Asn Pro Arg Arg Asn Phe Arg Ser Leu
95 100 105
Ile Glu Lys Lys Val Asn Glu Ile Lys Asp Asp Ser His Cys Gly
110 115 120
Glu Thr Phe Thr Gln Val Pro Asp Asp Arg Leu Asn Phe Gln Glu
125 130 135
Lys Lys Ala Ser Pro Glu Ile Lys Ser Cys Asp Ser Phe Val Cys

```
                140                           145                           150
Gly Glu Val Gly Leu Gly Asn Ser Ser Phe Asn Met Asn Ile Arg
                155                           160                           165
Gly Asp Ile Gly His Lys Ala Tyr Glu Tyr Gln Glu Tyr Gly Pro
                170                           175                           180
Lys Pro
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<210> 112
<211> 108
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:7762669.1.orf1:2002JAN18

<400> 112

```
Val Ser Thr Phe Leu Phe Trp Thr Tyr Gly Met Phe Gln Asp Ser
  1               5                  10                  15
Val Ala Phe Glu Asp Val Ala Val Asn Phe Thr His Glu Glu Trp
                 20                  25                  30
Ala Leu Leu Gly Pro Ser Gln Lys Asn Leu Tyr Arg Asp Val Met
                 35                  40                  45
Leu Glu Asn Phe Gln Asn Leu Ala Ser Leu Gly Tyr Pro Leu His
                 50                  55                  60
Thr Pro His Leu Ile Ser Gln Trp Glu Gln Glu Glu Asp Leu Gln
                 65                  70                  75
Thr Val Lys Arg Glu Leu Ile Gln Gly Ile Phe Met Gly Glu His
                 80                  85                  90
Arg Glu Gly Lys Asn Pro Trp Glu Lys Leu Phe Trp Leu Gly Glu
                 95                 100                 105
Lys Ile Asn
```

<210> 113
<211> 240
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:965822.1.orf1:2002JAN18

<400> 113

```
Pro Arg Ser Ser Arg Arg Val Trp Ala Ala Tyr Thr Glu Gly Lys
  1               5                  10                  15
Lys Lys Pro Ser Phe Leu Gly Lys Cys Arg Lys Pro Ala Ser Gly
                 20                  25                  30
Arg Ser Leu Arg Ser Pro Gln Gly Gly Ala Leu Ala Ala Gln Arg
                 35                  40                  45
Ala Arg Phe Pro Ala Gly Glu Pro Arg Asn Gly Gly Ala Gly Gly
                 50                  55                  60
Gly Asp Ser Glu Asp Pro Arg Leu Gly Phe Pro Thr Trp Ile Arg
                 65                  70                  75
Ser Ala Trp Gly Phe Asp Pro His Pro Gly Ala Ala Pro Arg Arg
                 80                  85                  90
Ser Trp Ala Ala Arg Ala Phe Gly Leu Arg His Arg Gln Arg His
                 95                 100                 105
Leu Glu Ala Gly Ala Ser Gly Arg Leu Cys Leu Thr Cys Leu Leu
                110                 115                 120
Glu Gly Asn Thr Gly Lys Pro Gly Leu Ala Val Thr Leu Val Thr
                125                 130                 135
```

```
Asn Met Ser Gln Asp Ser Val Thr Phe Ala Asp Val Ala Val Asn
                140                 145                 150
Phe Thr Lys Glu Glu Trp Thr Leu Leu Asp Pro Ala Gln Arg Asn
                155                 160                 165
Leu Tyr Arg Asp Val Met Leu Glu Asn Ser Arg Asn Leu Ala Phe
                170                 175                 180
Ile Asp Trp Ala Thr Pro Cys Lys Thr Lys Asp Ala Thr Pro Gln
                185                 190                 195
Pro Asp Ile Leu Pro Lys Arg Thr Phe Pro Glu Ala Asn Arg Val
                200                 205                 210
Cys Leu Thr Ser Ile Arg Phe Pro Ala Leu His Ile Lys Arg Arg
                215                 220                 225
Leu Glu Met Pro Gln Asn Arg Gly Thr Thr Gln Ala Gly Gly Glu
                230                 235                 240
```

<210> 114
<211> 319
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:006394.31.orf2:2002JAN18

<400> 114

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Gly Lys Arg Gly Leu Phe Ala Glu Gly Leu Gln Ala Met Pro Val
 1               5                  10                  15
Gly Ser Ala Phe Arg Val Pro Cys Pro Ile Leu Glu Gly Pro Ala
                20                  25                  30
Ala Gly Ser Arg Pro Arg Leu Ser Glu Ala Met Gly Ile Gln Ser
                35                  40                  45
Ala Glu Leu Pro Pro Glu Glu Ser Asp Ser Ser Arg Val Asp Phe
                50                  55                  60
Gly Ser Ser Glu Arg Leu Gly Ser Trp Gln Glu Lys Glu Glu Asp
                65                  70                  75
Ala Arg Pro Asn Ala Ala Ala Pro Ala Leu Gly Pro Val Gly Leu
                80                  85                  90
Glu Ser Asp Leu Ser Lys Val Arg His Lys Leu Arg Lys Phe Leu
                95                 100                 105
Gln Arg Arg Pro Thr Leu Gln Ser Leu Arg Glu Lys Gly Tyr Ile
                110                 115                 120
Lys Asp Gln Val Phe Gly Cys Ala Leu Ala Ala Leu Cys Glu Arg
                125                 130                 135
Glu Arg Ser Arg Val Pro Arg Phe Val Gln Gln Cys Ile Arg Ala
                140                 145                 150
Val Glu Ala Arg Gly Leu Asp Ile Asp Gly Leu Tyr Arg Ile Ser
                155                 160                 165
Gly Asn Leu Ala Thr Ile Gln Lys Leu Arg Tyr Lys Val Asp His
                170                 175                 180
Asp Glu Arg Leu Asp Leu Asp Asp Gly Arg Trp Glu Asp Val His
                185                 190                 195
Val Ile Thr Gly Ala Leu Lys Leu Phe Phe Arg Glu Leu Pro Glu
                200                 205                 210
Pro Leu Phe Pro Phe Ser His Phe Arg Gln Phe Ile Ala Ala Ile
                215                 220                 225
Lys Leu Gln Asp Gln Ala Arg Arg Ser Arg Cys Val Arg Asp Leu
                230                 235                 240
Val Arg Ser Leu Pro Ala Pro Asn His Asp Thr Leu Arg Met Leu
                245                 250                 255
Phe Gln His Leu Cys Arg Val Ile Glu His Gly Glu Gln Asn Arg
                260                 265                 270
Met Ser Val Gln Ser Val Ala Ile Val Phe Gly Pro Thr Leu Leu
```

```
Arg Pro Glu Val Glu Glu Thr Ser Met Pro Met Thr Met Val Phe
                275                 280                 285
Gln Asn Gln Val Val Glu Leu Ile Leu Gln Gln Cys Ala Asp Ile
                290                 295                 300
Phe Pro Pro His
                305                 310                 315
```

<210> 115
<211> 263
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:018258.1.orf2:2002JAN18

<400> 115

```
Gly Cys Asp Val Arg Leu Gln Thr Met Tyr Phe Leu Thr Pro Ile
 1               5                  10                  15
Leu Val Ala Ile Leu Cys Val Leu Val Val Trp Ile Phe Lys Asn
                20                  25                  30
Ala Asp Arg Ser Met Glu Lys Lys Lys Gly Glu Pro Arg Thr Arg
                35                  40                  45
Ala Glu Ala Arg Pro Trp Val Asp Glu Asp Leu Lys Asp Ser Ser
                50                  55                  60
Asp Leu His Gln Ala Glu Glu Asp Ala Asp Glu Trp Gln Glu Ser
                65                  70                  75
Glu Glu Asn Val Glu His Ile Pro Phe Ser His Asn His Tyr Pro
                80                  85                  90
Glu Lys Glu Met Val Lys Arg Ser Gln Glu Phe Tyr Glu Leu Leu
                95                 100                 105
Asn Lys Arg Arg Ser Val Arg Phe Ile Ser Asn Glu Gln Val Pro
               110                 115                 120
Met Glu Val Ile Asp Asn Val Ile Arg Thr Ala Gly Thr Ala Pro
               125                 130                 135
Ser Gly Ala His Thr Glu Pro Trp Thr Phe Val Val Val Lys Asp
               140                 145                 150
Pro Asp Val Lys His Lys Ile Arg Lys Ile Ile Glu Glu Glu Glu
               155                 160                 165
Glu Ile Asn Tyr Met Lys Arg Met Gly His Arg Trp Val Thr Asp
               170                 175                 180
Leu Lys Lys Leu Arg Thr Asn Trp Ile Lys Glu Tyr Leu Asp Thr
               185                 190                 195
Ala Pro Ile Leu Ile Leu Ile Phe Lys Gln Val His Gly Phe Ala
               200                 205                 210
Ala Asn Gly Lys Lys Lys Val His Tyr Tyr Asn Glu Ile Ser Val
               215                 220                 225
Ser Ile Ala Cys Gly His Pro Ala Ser Cys Pro Ala Glu Cys Ser
               230                 235                 240
Leu Val Thr Val Thr Asn Asn Pro Leu Asn Val Ala Ser Asp Glu
               245                 250                 255
Gly Cys Pro Trp Ala Ala Arg Thr
               260
```

<210> 116
<211> 449
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:027320.5.orf3:2002JAN18

<400> 116

Gly Glu Ala Gly Arg Ala Pro Asp Ser Asp Gly Gly Ser Asp Ala
1 5 10 15
Asp Ser Glu Val Gly Pro Gly Ser Pro Thr Arg Thr Ala Glu Ala
20 25 30
Ala Glu Glu Glu Met Ala Gly Pro Asn Gln Leu Cys Ile Arg Arg
35 40 45
Trp Thr Thr Lys His Val Ala Val Trp Leu Lys Asp Glu Gly Phe
50 55 60
Phe Glu Tyr Val Asp Ile Leu Cys Asn Lys His Arg Leu Asp Gly
65 70 75
Ile Thr Leu Leu Thr Leu Thr Glu Tyr Asp Leu Arg Ser Pro Pro
80 85 90
Leu Glu Ile Lys Val Leu Gly Asp Ile Lys Arg Leu Met Leu Ser
95 100 105
Val Arg Lys Leu Gln Lys Ile His Ile Asp Val Leu Glu Glu Met
110 115 120
Gly Tyr Asn Ser Asp Ser Pro Met Gly Ser Met Thr Pro Phe Ile
125 130 135
Ser Ala Leu Gln Ser Thr Asp Trp Leu Cys Asn Gly Glu Leu Ser
140 145 150
His Asp Cys Asp Gly Pro Ile Thr Asp Leu Asn Ser Asp Gln Tyr
155 160 165
Gln Tyr Met Asn Gly Lys Asn Lys His Ser Val Arg Arg Leu Asp
170 175 180
Pro Glu Tyr Trp Lys Thr Ile Leu Ser Cys Ile Tyr Val Phe Ile
185 190 195
Val Phe Gly Phe Thr Ser Phe Ile Met Val Ile Val His Glu Arg
200 205 210
Val Pro Asp Met Gln Thr Tyr Pro Pro Leu Pro Asp Ile Phe Leu
215 220 225
Asp Ser Val Pro Arg Ile Pro Trp Ala Phe Ala Met Thr Glu Val
230 235 240
Cys Gly Met Ile Leu Cys Tyr Ile Trp Leu Leu Val Leu Leu Leu
245 250 255
His Lys His Arg Ser Ile Leu Leu Arg Arg Leu Cys Ser Leu Met
260 265 270
Gly Thr Val Phe Leu Leu Arg Cys Phe Thr Met Phe Val Thr Ser
275 280 285
Leu Ser Val Pro Gly Gln His Leu Gln Cys Thr Gly Lys Ile Tyr
290 295 300
Gly Ser Val Trp Glu Lys Leu His Arg Ala Phe Ala Ile Trp Ser
305 310 315
Gly Phe Gly Met Thr Leu Thr Gly Val His Thr Cys Gly Asp Tyr
320 325 330
Met Phe Ser Gly His Thr Val Val Leu Thr Met Leu Asn Phe Phe
335 340 345
Val Thr Glu Tyr Thr Pro Arg Ser Trp Asn Phe Leu His Thr Leu
350 355 360
Ser Trp Val Leu Asn Leu Phe Gly Ile Phe Phe Ile Leu Ala Ala
365 370 375
His Glu His Tyr Ser Ile Asp Val Phe Ile Ala Phe Tyr Ile Thr
380 385 390
Thr Arg Leu Phe Leu Tyr Tyr His Thr Leu Ala Asn Thr Arg Ala
395 400 405
Tyr Gln Gln Ser Arg Arg Ala Arg Ile Trp Phe Pro Met Phe Ser
410 415 420
Phe Phe Glu Cys Asn Val Asn Gly Thr Val Pro Asn Glu Tyr Cys
425 430 435
Trp Pro Phe Ser Lys Pro Ala Ile Met Lys Arg Leu Ile Gly
440 445

<210> 117

<211> 601
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:057499.1.orf1:2002JAN18

<400> 117
Gln Gln His Pro Arg Gln Ala Ala Pro Gln Met Leu Gln Gln Gln
1 5 10 15
Pro Pro Arg Leu Ile Ser Val Gln Thr Met Gln Arg Gly Asn Met
20 25 30
Asn Cys Gly Ala Phe Gln Ala His Gln Met Arg Leu Ala Gln Asn
35 40 45
Ala Ala Arg Ile Pro Gly Ile Pro Arg His Ser Gly Pro Gln Tyr
50 55 60
Ser Met Met Gln Pro His Leu Gln Arg Gln His Ser Asn Pro Gly
65 70 75
His Ala Gly Pro Phe Pro Val Val Ser Val His Asn Thr Thr Ile
80 85 90
Asn Pro Thr Ser Pro Thr Thr Ala Thr Met Ala Asn Ala Asn Arg
95 100 105
Gly Pro Thr Ser Pro Ser Val Thr Ala Ile Glu Leu Ile Pro Ser
110 115 120
Val Thr Asn Pro Glu Asn Leu Pro Ser Leu Pro Asp Ile Pro Pro
125 130 135
Ile Gln Ala Asn Val Val Pro Met Met His Ser Trp Tyr Glu Phe
140 145 150
Gly Ala Arg Glu Lys Thr Gln Asp Gln Asn Val Leu Glu Asp Ala
155 160 165
Gly Ser Ser Ser Leu Asp Asn Leu Leu Ser Arg Tyr Ile Ser Gly
170 175 180
Ser His Leu Pro Pro Gln Pro Thr Ser Thr Met Asn Pro Ser Pro
185 190 195
Gly Pro Ser Ala Leu Ser Pro Gly Ser Ser Gly Leu Ser Asn Ser
200 205 210
His Thr Pro Val Arg Pro Pro Ser Thr Ser Ser Thr Gly Ser Arg
215 220 225
Gly Ser Cys Gly Ser Ser Gly Arg Thr Ala Glu Lys Thr Ser Leu
230 235 240
Ser Phe Lys Ser Asp Gln Val Lys Val Lys Gln Glu Pro Gly Thr
245 250 255
Glu Asp Glu Ile Cys Ser Phe Ser Gly Gly Val Lys Gln Glu Lys
260 265 270
Thr Glu Asp Gly Arg Arg Ser Ala Cys Met Leu Ser Ser Pro Glu
275 280 285
Ser Ser Leu Thr Pro Pro Leu Ser Thr Asn Leu His Leu Glu Ser
290 295 300
Glu Leu Asp Ala Leu Ala Ser Leu Glu Asn His Val Lys Ile Glu
305 310 315
Pro Ala Asp Met Asn Glu Ser Cys Lys Gln Ser Gly Leu Ser Ser
320 325 330
Leu Val Asn Gly Lys Ser Pro Ile Arg Ser Leu Met His Arg Ser
335 340 345
Ala Arg Ile Gly Gly Asp Gly Asn Asn Lys Asp Asp Asp Pro Asn
350 355 360
Glu Asp Trp Cys Ala Val Cys Gln Asn Gly Gly Asp Leu Leu Cys
365 370 375
Cys Glu Lys Cys Pro Lys Val Phe His Leu Thr Cys His Val Pro
380 385 390
Thr Leu Leu Ser Phe Pro Ser Gly Asp Trp Ile Cys Thr Phe Cys
395 400 405

Arg Asp Ile Gly Lys Pro Glu Val Glu Tyr Asp Cys Asp Asn Leu
410 415 420
Gln His Ser Lys Lys Gly Lys Thr Ala Gln Gly Leu Ser Pro Val
425 430 435
Asp Gln Arg Lys Cys Glu Arg Leu Leu Leu Tyr Leu Tyr Cys His
440 445 450
Glu Leu Ser Ile Glu Phe Gln Glu Pro Val Pro Ala Ser Ile Pro
455 460 465
Asn Tyr Tyr Lys Ile Ile Lys Lys Pro Met Asp Leu Ser Thr Val
470 475 480
Lys Lys Lys Leu Gln Lys Lys His Ser Gln His Tyr Gln Ile Pro
485 490 495
Asp Asp Phe Val Ala Asp Val Arg Leu Ile Phe Lys Asn Cys Glu
500 505 510
Arg Phe Asn Glu Met Met Lys Val Val Gln Val Tyr Ala Asp Thr
515 520 525
Gln Glu Ile Asn Leu Lys Ala Asp Ser Glu Val Ala Gln Ala Gly
530 535 540
Lys Ala Val Ala Leu Tyr Phe Glu Asp Lys Leu Thr Glu Ile Tyr
545 550 555
Ser Asp Arg Thr Phe Ala Pro Leu Pro Glu Phe Glu Gln Glu Glu
560 565 570
Asp Asp Gly Glu Val Thr Glu Asp Ser Asp Glu Asp Phe Ile Gln
575 580 585
Pro Arg Arg Lys Arg Leu Lys Ser Asp Glu Arg Pro Val His Ile
590 595 600
Lys

<210> 118
<211> 170
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:065935.21.orf2:2002JAN18

<400> 118
Phe Leu His Tyr His Pro Pro Pro Thr Gln Gly Trp Trp Trp Arg
1 5 10 15
Lys Met Ala Ala Ala Trp Gly Ser Ser Leu Thr Ala Ala Thr Gln
20 25 30
Arg Ala Val Thr Pro Trp Pro Arg Gly Arg Leu Leu Thr Ala Ser
35 40 45
Leu Gly Pro Gln Ala Arg Arg Glu Ala Ser Ser Ser Ser Pro Glu
50 55 60
Ala Gly Glu Gly Gln Ile Arg Leu Thr Asp Ser Cys Val Gln Arg
65 70 75
Leu Leu Glu Ile Thr Glu Gly Ser Glu Phe Leu Arg Leu Gln Val
80 85 90
Glu Gly Gly Gly Cys Ser Gly Phe Gln Tyr Lys Phe Ser Leu Asp
95 100 105
Thr Val Ile Asn Pro Asp Asp Arg Val Phe Glu Gln Gly Gly Ala
110 115 120
Arg Val Val Val Asp Ser Asp Ser Leu Ala Phe Val Lys Gly Ala
125 130 135
Gln Val Asp Phe Ser Gln Glu Leu Ile Arg Ser Ser Phe Gln Val
140 145 150
Leu Asn Asn Pro Gln Ala Gln Gln Gly Cys Ser Cys Gly Ser Ser
155 160 165
Phe Ser Ile Lys Leu
170

<210> 119
<211> 106
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:071860.12.orf3:2002JAN18

<400> 119
Val Cys Arg Asn Ser Tyr Phe Tyr Leu Pro Ser Leu Ser Glu Ser
1 5 10 15
Lys His Cys Leu Arg Ile Gln His Thr Phe Cys Phe Leu Thr Cys
20 25 30
Val Gln Ala Tyr Val His Lys Ser Val Met Glu Glu Leu Lys Arg
35 40 45
Ile Ile Asp Asp Ser Glu Ile Thr Lys Glu Asp Asp Ala Leu Trp
50 55 60
Pro Pro Pro Asp Arg Val Gly Arg Gln Glu Leu Glu Ile Val Ile
65 70 75
Gly Asp Glu His Ile Ser Phe Thr Thr Ser Lys Ile Gly Ser Leu
80 85 90
Ile Asp Val Asn Gln Ser Lys Asp Pro Glu Gly Leu Arg Val Phe
95 100 105
Tyr

<210> 120
<211> 334
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:087383.29.orf2:2002JAN18

<400> 120
Val Tyr Phe Ala Ala Pro Ser Ala Phe Glu Lys Met Ser Val Thr
1 5 10 15
Tyr Asp Asp Ser Val Gly Val Glu Val Ser Ser Asp Ser Phe Trp
20 25 30
Glu Val Gly Asn Tyr Lys Arg Thr Val Lys Arg Ile Asp Asp Gly
35 40 45
His Arg Leu Cys Ser Asp Leu Met Asn Cys Leu His Glu Arg Ala
50 55 60
Arg Ile Glu Lys Ala Tyr Ala Gln Gln Leu Thr Glu Trp Ala Arg
65 70 75
Arg Trp Arg Gln Leu Val Glu Lys Gly Pro Gln Tyr Gly Thr Val
80 85 90
Glu Lys Ala Trp Met Ala Phe Met Ser Glu Ala Glu Arg Val Ser
95 100 105
Glu Leu His Leu Glu Val Lys Ala Ser Leu Met Asn Asp Asp Phe
110 115 120
Glu Lys Ile Lys Asn Trp Gln Lys Glu Ala Phe His Lys Gln Met
125 130 135
Met Gly Gly Phe Lys Glu Thr Lys Glu Ala Glu Asp Gly Phe Arg
140 145 150
Lys Ala Gln Lys Pro Trp Ala Lys Lys Leu Lys Glu Val Glu Ala
155 160 165
Ala Lys Lys Ala His His Ala Ala Cys Lys Glu Glu Lys Leu Ala
170 175 180
Ile Ser Arg Glu Ala Asn Ser Lys Ala Asp Pro Ser Leu Asn Pro
185 190 195

Glu Gln Leu Lys Lys Leu Gln Asp Lys Ile Glu Lys Cys Lys Gln
200 205 210
Asp Val Leu Lys Thr Lys Glu Lys Tyr Glu Lys Ser Leu Lys Glu
215 220 225
Leu Asp Gln Gly Thr Pro Gln Tyr Met Glu Asn Met Glu Gln Val
230 235 240
Phe Glu Gln Cys Gln Gln Phe Glu Glu Lys Arg Leu Arg Phe Phe
245 250 255
Arg Glu Val Leu Leu Glu Val Gln Lys His Leu Asp Leu Ser Asn
260 265 270
Val Ala Gly Tyr Lys Ala Ile Tyr His Asp Leu Glu Gln Ser Ile
275 280 285
Arg Ala Ala Asp Ala Val Glu Asp Leu Arg Trp Phe Arg Ala Asn
290 295 300
His Gly Pro Gly Met Ala Met Asn Trp Pro Gln Phe Glu Val Arg
305 310 315
Gly Gly Cys Ala His Glu Leu Val Ser Leu Glu Glu Asp Leu Gly
320 325 330
Pro Gln Ser Cys

<210> 121
<211> 109
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:098580.3.orf2:2002JAN18

<400> 121
Gln Trp Lys Lys Pro Val Gln Ile Leu Met Val Gly Ser Cys Lys
1 5 10 15
Val Thr Ser Val Met Met Leu Leu Gln Arg Leu Met Trp Glu Lys
20 25 30
Asp Phe Ile Ala Phe Lys Ser Ser Thr Pro His Asn Val Ser Trp
35 40 45
Arg His Glu Thr Asn Gly Ser Val Phe Ile Ser Gln Ile Ile Tyr
50 55 60
Tyr Phe Arg Glu Tyr Ser Trp Ser His His Leu Glu Glu Ile Phe
65 70 75
Gln Lys Val Gln His Ser Phe Glu Thr Pro Asn Ile Leu Thr Gln
80 85 90
Leu Pro Thr Ile Glu Arg Leu Ser Met Thr Arg Tyr Phe Tyr Leu
95 100 105
Phe Pro Gly Asn

<210> 122
<211> 519
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:1001879.1.orf1:2002JAN18

<400> 122
Arg Ala Ala Val Leu Gly Arg Val Arg Gly Gly Leu Ala Ala Glu
1 5 10 15
Ala Pro Arg Arg Gly Ala Asn Gly Ala Asn Ala Ala Arg Ser Pro
20 25 30
Pro Ala Arg Arg Cys Ala Gly Gly Trp Trp Arg Gly Pro Arg Pro

35 40 45
Thr Leu Arg Thr Met Thr Cys Trp Leu Cys Val Leu Ser Leu Pro
50 55 60
Leu Leu Leu Leu Pro Ala Ala Pro Pro Pro Ala Gly Gly Cys Pro
65 70 75
Ala Arg Cys Glu Cys Thr Val Gln Thr Arg Ala Val Ala Cys Thr
80 85 90
Arg Arg Arg Leu Thr Ala Val Pro Asp Gly Ile Pro Ala Glu Thr
95 100 105
Arg Leu Leu Glu Leu Ser Arg Asn Arg Ile Arg Cys Leu Asn Pro
110 115 120
Gly Asp Leu Ala Ala Leu Pro Ala Leu Glu Glu Leu Asp Leu Ser
125 130 135
Glu Asn Ala Ile Ala His Val Glu Pro Gly Ala Phe Ala Asn Leu
140 145 150
Pro Arg Leu Arg Val Leu Arg Leu Arg Gly Asn Gln Leu Lys Leu
155 160 165
Ile Pro Pro Gly Val Phe Thr Arg Leu Asp Asn Leu Thr Leu Leu
170 175 180
Asp Leu Ser Glu Asn Lys Leu Val Ile Leu Leu Asp Tyr Thr Phe
185 190 195
Gln Asp Leu His Ser Leu Arg Arg Leu Glu Val Gly Asp Asn Asp
200 205 210
Leu Val Phe Val Ser Arg Arg Ala Phe Ala Gly Leu Leu Ala Leu
215 220 225
Glu Glu Leu Thr Leu Glu Arg Cys Asn Leu Thr Ala Leu Ser Gly
230 235 240
Glu Ser Leu Gly His Leu Arg Ser Leu Gly Ala Leu Arg Leu Arg
245 250 255
His Leu Ala Ile Ala Ser Leu Glu Asp Gln Asn Phe Arg Arg Leu
260 265 270
Pro Gly Leu Leu His Leu Glu Ile Ala Gln Leu Ala Ala Ala Gly
275 280 285
Arg Gln Val Ala Ala Gly Ser Leu Arg Gly Leu Asn Leu Thr Ser
290 295 300
Leu Ser Val Thr His Thr Asn Ile Thr Ala Val Pro Ala Ala Ala
305 310 315
Leu Arg His Gln Ala His Leu Thr Cys Leu Asn Leu Ser His Asn
320 325 330
Pro Ile Ser Thr Val Pro Arg Gly Ser Phe Arg Asp Leu Val Arg
335 340 345
Leu Arg Glu Leu His Leu Ala Gly Ala Leu Leu Ala Val Val Glu
350 355 360
Pro Gln Ala Phe Leu Gly Leu Arg Gln Ile Arg Leu Leu Asn Leu
365 370 375
Ser Asn Asn Leu Leu Ser Thr Leu Glu Glu Ser Thr Phe His Ser
380 385 390
Val Asn Thr Leu Glu Thr Leu Arg Val Asp Gly Asn Pro Leu Ala
395 400 405
Cys Asp Cys Arg Leu Leu Trp Ile Val Gln Arg Arg Lys Thr Leu
410 415 420
Asn Phe Asp Gly Arg Leu Pro Ala Cys Ala Thr Pro Ala Glu Val
425 430 435
Arg Gly Asp Ala Leu Arg Asn Leu Pro Asp Ser Val Leu Phe Glu
440 445 450
Tyr Phe Val Cys Arg Lys Pro Lys Ile Arg Glu Arg Arg Leu Gln
455 460 465
Arg Val Thr Ala Thr Ala Gly Glu Asp Val Arg Phe Leu Cys Arg
470 475 480
Ala Glu Gly Glu Pro Ala Pro Thr Val Ala Trp Val Thr Pro Gln
485 490 495
His Arg Pro Val Thr Ala Thr Ser Ala Gly Arg Ala Arg Val Leu
500 505 510

Pro Gly Gly Thr Leu Glu Ile Gln Asp
515

<210> 123
<211> 132
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:1079456.4.orf3:2002JAN18

<400> 123
Gly Asp Pro Pro Arg Pro Gly Phe Cys Pro Ala Arg Ala Asp Ser
1 5 10 15
Arg Lys Ser Gly Ser Gly Ser Arg Gly Val Thr Val Thr Pro Arg
20 25 30
Arg Ile Asn Ser Gln Arg Leu Met Leu His Glu Lys Ala Thr Lys
35 40 45
Lys Thr Lys Glu Lys Glu Thr Arg Met Ala Leu Pro Gln Gly Cys
50 55 60
Leu Thr Phe Lys Asp Val Ala Ile Glu Phe Ser Leu Glu Glu Trp
65 70 75
Lys Cys Leu Asn Pro Ala Gln Arg Ala Leu Tyr Arg Ala Val Met
80 85 90
Leu Glu Asn Tyr Arg Asn Leu Glu Ser Val Gly Leu Thr Ser Lys
95 100 105
Asp Ser Trp Tyr Met Arg Lys Lys Pro Gly Arg Gly Arg Gly Lys
110 115 120
Gln Arg Arg Gln Glu Trp Phe Phe Leu Arg Val Tyr
125 130

<210> 124
<211> 524
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:1080598.9.orf2:2002JAN18

<400> 124
Pro Cys Thr Lys Arg Asn Gly Asp Cys Leu Tyr Pro Pro Arg Phe
1 5 10 15
Ile Ser Trp Pro Glu Val Ile Leu Ala Ser Arg Lys Gly Cys Thr
20 25 30
Ser Ser His His Gln Leu Gln Arg Met Ala Ala Ile Tyr Leu Ser
35 40 45
Arg Gly Phe Phe Ser Arg Glu Pro Ile Cys Pro Phe Glu Glu Lys
50 55 60
Thr Lys Val Glu Arg Met Val Glu Asp Tyr Leu Ala Ser Gly Tyr
65 70 75
Gln Asp Ser Val Thr Phe Asp Asp Val Ala Val Asp Phe Thr Pro
80 85 90
Glu Glu Trp Ala Leu Leu Asp Thr Thr Glu Lys Tyr Leu Tyr Arg
95 100 105
Asp Val Met Leu Glu Asn Tyr Met Asn Leu Ala Ser Val Glu Trp
110 115 120
Glu Ile Gln Pro Arg Thr Lys Arg Ser Ser Leu Gln Gln Gly Phe
125 130 135
Leu Lys Asn Gln Ile Phe Ser Gly Ile Gln Met Thr Arg Gly Tyr
140 145 150
Ser Gly Trp Lys Leu Cys Asp Cys Lys Asn Cys Gly Glu Val Phe

155 160 165
Arg Glu Gln Phe Cys Leu Lys Thr His Met Arg Val Gln Asn Gly
170 175 180
Gly Asn Thr Ser Glu Gly Asn Cys Tyr Gly Lys Asp Thr Leu Ser
185 190 195
Val His Lys Glu Ala Ser Thr Gly Gln Glu Leu Ser Lys Phe Asn
200 205 210
Pro Cys Gly Lys Val Phe Thr Leu Thr Pro Gly Leu Ala Val His
215 220 225
Leu Glu Val Leu Asn Ala Arg Gln Pro Tyr Lys Cys Lys Glu Cys
230 235 240
Gly Lys Gly Phe Lys Tyr Phe Ala Ser Leu Asp Asn His Met Gly
245 250 255
Ile His Thr Asp Glu Lys Leu Cys Glu Phe Gln Glu Tyr Gly Arg
260 265 270
Ala Val Thr Ala Ser Ser His Leu Lys Gln Cys Val Ala Val His
275 280 285
Thr Gly Lys Lys Ser Lys Lys Thr Lys Lys Cys Gly Lys Ser Phe
290 295 300
Thr Asn Phe Ser Gln Leu Tyr Ala Pro Val Lys Thr His Lys Gly
305 310 315
Glu Lys Ser Phe Glu Cys Lys Glu Cys Gly Arg Ser Phe Arg Asn
320 325 330
Ser Ser Cys Leu Asn Asp His Ile Gln Ile His Thr Gly Ile Lys
335 340 345
Pro His Lys Cys Thr Tyr Cys Gly Lys Ala Phe Thr Arg Ser Thr
350 355 360
Gln Leu Thr Glu His Val Arg Thr His Thr Gly Ile Lys Pro Tyr
365 370 375
Glu Cys Lys Glu Cys Gly Gln Ala Phe Ala Gln Tyr Ser Gly Leu
380 385 390
Ser Ile His Ile Arg Ser His Ser Gly Lys Lys Pro Tyr Gln Cys
395 400 405
Lys Glu Cys Gly Lys Ala Phe Thr Thr Ser Thr Ser Leu Ile Gln
410 415 420
His Thr Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Val Glu
425 430 435
Cys Gly Lys Thr Phe Ile Thr Ser Ser Arg Arg Ser Lys His Leu
440 445 450
Lys Thr His Ser Gly Glu Lys Pro Phe Val Cys Lys Ile Cys Gly
455 460 465
Lys Ala Phe Leu Tyr Ser Ser Arg Leu Asn Val His Leu Arg Thr
470 475 480
His Thr Gly Glu Lys Pro Phe Val Cys Lys Glu Cys Gly Lys Ala
485 490 495
Phe Ala Val Ser Ser Arg Leu Ser Arg His Glu Arg Ile His Thr
500 505 510
Gly Glu Lys Pro Tyr Glu Cys Lys Asp Met Ser Val Thr Ile
515 520

<210> 125
<211> 309
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:1090358.10.orf1:2002JAN18

<400> 125
Asn Ser Tyr Leu Leu Leu Arg His Ser Phe Asn Cys Gly Leu Phe
1 5 10 15
Val Val Val Val Phe Gln Gly Arg Ser Pro Arg Lys Ile Asp Gln

```
                    20                       25                       30
Phe Cys Asn Ser Ser Asn Met Val His Gly Ser Val Thr Phe Arg
                    35                       40                       45
Asp Val Ala Ile Asp Phe Ser Gln Glu Glu Trp Glu Cys Leu Gln
                    50                       55                       60
Pro Asp Gln Arg Thr Leu Tyr Arg Asp Val Met Leu Glu Asn Tyr
                    65                       70                       75
Ser His Leu Ile Ser Leu Gly Ser Ser Ile Ser Lys Pro Asp Val
                    80                       85                       90
Ile Thr Leu Leu Glu Gln Glu Lys Glu Pro Trp Met Val Val Arg
                    95                       100                      105
Lys Glu Thr Ser Arg Arg Tyr Pro Asp Leu Glu Leu Lys Tyr Gly
                    110                      115                      120
Pro Glu Lys Val Ser Pro Glu Asn Asp Thr Ser Glu Val Asn Leu
                    125                      130                      135
Pro Lys Gln Val Ile Lys Gln Ile Ser Thr Thr Leu Gly Ile Glu
                    140                      145                      150
Ala Phe Tyr Phe Arg Asn Asp Ser Glu Tyr Arg Gln Phe Glu Gly
                    155                      160                      165
Leu Gln Gly Tyr Gln Glu Gly Asn Ile Asn Gln Lys Met Ile Ser
                    170                      175                      180
Tyr Glu Lys Leu Pro Thr His Thr Pro His Ala Ser Leu Ile Cys
                    185                      190                      195
Asn Thr His Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys Tyr Phe
                    200                      205                      210
Ser Arg Ser Ala Asn Leu Ile Gln His Gln Ser Ile His Thr Gly
                    215                      220                      225
Glu Lys Pro Phe Glu Cys Lys Glu Cys Gly Lys Ala Phe Arg Leu
                    230                      235                      240
His Ile Gln Phe Thr Arg His Gln Lys Phe His Thr Gly Glu Lys
                    245                      250                      255
Pro Leu Asn Val Thr Asn Val Glu Arg Pro Leu Val Phe Leu Pro
                    260                      265                      270
Cys Leu Ile Ala Ile Arg Thr Phe Thr Gln Val Arg Asn Cys Leu
                    275                      280                      285
Asn Val Arg Asn Val Gly Ser Pro Leu Ile Val Ala Gln Thr Leu
                    290                      295                      300
Phe Asn Ile Arg Val Phe Ile Leu Val
                    305
```

<210> 126
<211> 339
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:1097492.2.orf2:2002JAN18

<400> 126

```
Ala Arg Phe Pro Gly Ser Thr Gly Tyr Ile Trp Pro Lys Ser Asp
1               5                   10                  15
Ser Leu Gly Ala Leu Val His Ser Pro Val Asn Cys Pro Leu Leu
                20                  25                  30
Gly Phe Ser Ala Val Ser Thr Ser Leu Pro Gln Gly Tyr Leu Trp
                35                  40                  45
Val Gly Gly Gly Gln Glu Gly Ala Gly Gly Gln Val Glu Ile Phe
                50                  55                  60
Ser Leu Asn Arg Pro Ser Pro Arg Thr Val Lys Ser Phe Pro Leu
                65                  70                  75
Ala Ala Pro Val Leu Cys Met Glu Tyr Ile Pro Glu Leu Glu Glu
                80                  85                  90
Glu Ala Glu Ser Arg Asp Glu Ser Pro Thr Val Ala Asp Pro Ser
```

Ala Thr Val His Pro Thr Ile Cys Leu Gly Leu Gln Asp Gly Ser
95 100 105
Ile Leu Leu Tyr Ser Ser Val Asp Thr Gly Thr Gln Cys Leu Val
110 115 120
Ser Cys Arg Ser Pro Gly Leu Gln Pro Val Leu Cys Leu Arg His
125 130 135
Ser Pro Phe His Leu Leu Ala Gly Leu Gln Asp Gly Thr Leu Ala
140 145 150
Ala Tyr Pro Arg Thr Ser Gly Gly Val Leu Trp Asp Leu Glu Ser
155 160 165
Pro Pro Val Cys Leu Thr Val Gly Pro Gly Pro Val Arg Thr Leu
170 175 180
Leu Ser Leu Glu Asp Ala Val Trp Ala Ser Cys Gly Pro Arg Val
185 190 195
Thr Val Leu Glu Ala Thr Thr Leu Gln Pro Gln Gln Ser Phe Glu
200 205 210
Ala His Gln Asp Glu Ala Val Ser Val Thr His Met Val Lys Ala
215 220 225
Gly Ser Gly Val Trp Met Ala Phe Ser Ser Gly Thr Ser Ile Arg
230 235 240
Leu Phe His Thr Glu Thr Leu Glu His Leu Gln Glu Ile Asn Ile
245 250 255
Ala Thr Arg Thr Thr Phe Leu Leu Pro Gly Gln Lys His Leu Cys
260 265 270
Val Thr Ser Leu Leu Ile Cys Gln Gly Leu Leu Trp Val Gly Thr
275 280 285
Asp Gln Gly Val Ile Val Leu Leu Pro Val Pro Arg Leu Glu Gly
290 295 300
Ile Pro Lys Ile Thr Gln Trp Ala Leu Trp Ala Cys Gly Leu Pro
305 310 315
Gly Cys Gly Tyr Gln His Pro Gly Pro
320 325 330
335

<210> 127
<211> 163
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:1099945.26.orf2:2002JAN18

<400> 127
Glu Ala Arg Pro Ile Leu Ser Leu Ser His Thr Leu Thr His Leu
1 5 10 15
Thr Cys Trp Leu Val Thr Ser Lys Asp Thr Pro Ile Cys Leu Ala
20 25 30
Pro Trp Leu Ala Ala Ala Pro Thr His Pro Cys Pro Pro Pro Ala
35 40 45
Gln Ala Pro Asp Pro Lys Glu Glu Val Glu Gly Ala Cys Pro Pro
50 55 60
Leu Ser Ala Met Gln His Leu Leu Glu Ala Ala Gln Ser Leu Leu
65 70 75
Thr Ser Val Pro His Leu Ser His Arg Met Gln Lys Met Thr Ser
80 85 90
Lys Ala Tyr His Leu Gln Lys Ser Thr Cys Gly Lys Cys Gly Tyr
95 100 105
Pro Ala Lys Arg Lys Arg Lys Tyr Asn Trp Ser Ala Lys Ala Lys
110 115 120
Arg Arg Asn Thr Thr Gly Thr Gly Arg Met Arg His Leu Lys Ile
125 130 135
Val Tyr Arg Arg Phe Arg His Gly Phe Arg Glu Gly Thr Thr Pro

Lys Pro Lys Arg Ala Ala Val Ala Ala Ser Ser Ser Ser
140 145 150
155 160

<210> 128
<211> 352
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:110016.1.orf1:2002JAN18

<400> 128
Pro Ser Arg Ser Ala Arg Ala Ser Cys Thr Trp Arg Arg Cys Pro
1 5 10 15
Arg Thr Trp Trp Pro Arg Cys Cys Thr Thr Cys Thr His Gln Arg
20 25 30
Ser Arg Trp Met Arg Arg Ala Cys Arg Ile Cys Ser Pro Arg His
35 40 45
Thr Ala Ser Arg Ser Leu Pro Ser Ser Pro Ser Ala Cys Pro Ser
50 55 60
Cys Arg Ser Ala Cys Ala Ser Pro Thr Ala Trp Pro Ser Ser Val
65 70 75
Ser Ala Ser Cys Ser Thr Ala Arg Val Ser Pro Trp Leu Pro Ala
80 85 90
Thr Ser Ser Ala Leu Thr Ser Arg Trp Trp Arg Ala Thr Leu Thr
95 100 105
Ser Ser Asp Ser Arg Arg Arg Ala His Arg His His Leu Gln Arg
110 115 120
Arg Ala Leu Thr Trp Arg Arg Arg Ser Leu Val Phe Glu Ala Val
125 130 135
Met Arg Trp Ala Gly Ser Gly Asp Ala Glu Ala Gln Ala Glu Arg
140 145 150
Gln Arg Ala Leu Pro Thr Val Phe Glu Ser Val Arg Cys Arg Leu
155 160 165
Leu Pro Arg Ala Phe Leu Glu Ser Arg Val Glu Arg His Pro Leu
170 175 180
Val Arg Ala Gln Pro Glu Leu Leu Arg Lys Val Gln Met Val Lys
185 190 195
Asp Ala His Glu Gly Arg Ile Thr Thr Leu Arg Lys Lys Lys Lys
200 205 210
Gly Lys Asp Gly Ala Gly Ala Lys Glu Ala Asp Lys Gly Thr Ser
215 220 225
Lys Ala Lys Ala Glu Glu Asp Glu Glu Ala Glu Arg Ile Leu Pro
230 235 240
Gly Ile Leu Asn Asp Thr Leu Arg Phe Gly Met Phe Leu Gln Asp
245 250 255
Leu Ile Phe Met Ile Ser Glu Glu Gly Ala Val Ala Tyr Asp Pro
260 265 270
Ala Ala Asn Glu Cys Tyr Cys Ala Ser Leu Ser Ser Gln Val Pro
275 280 285
Lys Asn His Val Ser Leu Val Thr Lys Glu Asn Gln Val Phe Val
290 295 300
Ala Gly Gly Leu Phe Tyr Asn Glu Asp Asn Lys Glu Asp Pro Met
305 310 315
Ser Ala Tyr Phe Leu Gln Phe Asp His Leu Val Gly Gly Gln Arg
320 325 330
Asp Gln Gly Arg Arg Ala Leu Pro Gly Leu Gly His Val Leu Arg
335 340 345
Gln Ala Val Ile Gln Met Gly
350

<210> 129
<211> 138
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:1137613.10.orf2:2002JAN18

<220>
<221> unsure
<222> (1) ... (138)
<223> unknown or other

<400> 129
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Arg Thr His Gln Leu Asn Asn Ile Pro His Val Ala Asp Thr Asn
 1               5                  10                  15
Lys Ala Ala Val Ser Ser Phe Ser Lys Pro Leu Lys Gly Ser Ala
                20                  25                  30
Gly Gly Arg Arg Asn Ser Lys Gly Gly Pro Arg Gln Gly Ala Ile
                35                  40                  45
Gly Leu Gly Leu Arg Glu Pro Glu Thr Ala Ala Ala Ala Ala Ala
                50                  55                  60
Ala Ala Ala Gly Gly Ala Gln Gly Thr Pro Xaa Leu Pro Val Leu
                65                  70                  75
Cys Leu Gly Pro Ser Leu Leu Pro Arg Ala Gln Cys Gly Leu Ala
                80                  85                  90
Ser Val Lys Glu Phe Asp Lys Lys Tyr Asn Pro Thr Trp His Cys
                95                 100                 105
Ile Val Gly Arg Asn Phe Gly Ser Tyr Val Thr His Glu Thr Lys
               110                 115                 120
His Phe Ile Tyr Phe Tyr Leu Gly Gln Val Ala Ile Leu Leu Phe
               125                 130                 135
Lys Ser Gly
```

<210> 130
<211> 608
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:118836.26.orf2:2002JAN18

<400> 130
```
Gly Arg Leu Ser Ser Gln Pro Trp Met Phe Ser Ser Cys Gly Arg
 1               5                  10                  15
Pro Ala Ser Lys Ser Thr Thr Ser Ser Thr Pro Arg Thr Arg Gln
                20                  25                  30
Leu His Ala Trp Ser Arg Cys Trp Asn Gly Ala Phe Thr Pro Cys
                35                  40                  45
Arg Leu Ser Ala Ser Pro Ala Thr Asn Ala Thr Arg Trp Gly Met
                50                  55                  60
Ala Ala Pro Arg Cys Trp Ser Arg Pro Cys Arg Glu Thr Leu Ser
                65                  70                  75
Trp Ser Trp Arg Ala Ala Pro Trp Pro Leu Ser Pro Thr Gly Thr
                80                  85                  90
Ala Ser Trp Lys Pro Val Cys Leu Phe Pro Arg Pro Pro Gly Lys
                95                 100                 105
Thr Ala Pro Ala Arg Ala Val Pro Ser Arg Met Cys Ser Arg Pro
               110                 115                 120
Thr Met Gln Pro Ser Lys Ser Met Ala Pro Pro Pro Arg Arg Ala
```

```
                125                     130                     135
Leu Pro Leu Pro Val Val Ala Ser Ala Glu Pro Val Arg Ser Ala
                140                     145                     150
Ser Pro Ala Arg Cys Gln Ala Trp Leu Arg Ala Thr Arg His Pro
                155                     160                     165
Ala Ser Pro Arg Ser Leu Gln Ser Gly Gly Ala Arg Ser Gly Ser
                170                     175                     180
Thr Thr Pro Cys Thr Ala Leu Thr Pro Ser Thr Ala Phe Pro Thr
                185                     190                     195
Val Ala Leu Pro His Leu Phe His Ala Ser Tyr Trp Glu Ser Thr
                200                     205                     210
Asp Val Val Ser Phe Leu Leu Arg Gln Val Met Arg His Asp Asn
                215                     220                     225
Ser Ser Ile Leu Glu Leu Asp Gly Lys Glu Val Ser Val Phe Thr
                230                     235                     240
Pro Ser Lys Pro Arg Glu Lys Trp Gln Arg Lys Arg Thr His Val
                245                     250                     255
Lys Leu Arg Asn Val Thr Ala Asn His Arg Ile Asn Asp Ala Leu
                260                     265                     270
Ala Asn Glu Asp Gly Pro Gln Val Leu Thr Gly Arg Phe Met Tyr
                275                     280                     285
Gly Pro Leu Asp Met Val Thr Leu Thr Gly Glu Lys Val Asp Val
                290                     295                     300
His Ile Met Thr Gln Pro Pro Ser Gly Glu Trp Leu Tyr Leu Asp
                305                     310                     315
Thr Leu Val Thr Asn Asn Ser Gly Arg Val Ser Tyr Thr Ile Pro
                320                     325                     330
Glu Ser His Arg Leu Gly Val Gly Val Tyr Pro Ile Lys Met Val
                335                     340                     345
Val Arg Gly Asp His Thr Phe Ala Asp Ser Tyr Ile Thr Val Leu
                350                     355                     360
Pro Lys Gly Thr Glu Phe Val Val Phe Ser Ile Asp Gly Ser Phe
                365                     370                     375
Ala Ala Ser Val Ser Ile Met Gly Ser Asp Pro Lys Val Arg Ala
                380                     385                     390
Gly Ala Val Asp Val Val Arg His Trp Gln Asp Leu Gly Tyr Leu
                395                     400                     405
Ile Ile Tyr Val Thr Gly Arg Pro Asp Met Gln Lys Gln Arg Val
                410                     415                     420
Val Ala Trp Leu Ala Gln His Asn Phe Pro His Gly Val Val Ser
                425                     430                     435
Phe Cys Asp Gly Leu Val His Asp Pro Leu Arg His Lys Ala Asn
                440                     445                     450
Phe Leu Lys Leu Leu Ile Ser Glu Leu His Leu Arg Val His Ala
                455                     460                     465
Ala Tyr Gly Ser Thr Lys Asp Val Ala Val Tyr Ser Ala Ile Ser
                470                     475                     480
Leu Ser Pro Met Gln Ile Tyr Ile Val Gly Arg Pro Thr Lys Lys
                485                     490                     495
Leu Gln Gln Gln Cys Gln Phe Ile Thr Asp Gly Tyr Ala Ala His
                500                     505                     510
Leu Ala Gln Leu Lys Tyr Ser His Arg Ala Arg Pro Ala Arg Asn
                515                     520                     525
Thr Ala Thr Arg Met Ala Leu Arg Lys Gly Ser Phe Gly Leu Pro
                530                     535                     540
Gly Gln Gly Asp Phe Leu Arg Ser Arg Asn His Leu Leu Arg Thr
                545                     550                     555
Ile Ser Ala Gln Pro Ser Gly Pro Ser His Arg His Glu Arg Thr
                560                     565                     570
Gln Ser Gln Ala Asp Gly Glu Gln Arg Gly Gln Arg Ser Met Ser
                575                     580                     585
Val Ala Ala Gly Cys Trp Gly Arg Ala Met Thr Gly Arg Leu Glu
                590                     595                     600
```

Pro Gly Ala Ala Ala Gly Pro Lys
605

<210> 131
<211> 694
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:1330261.32.orf1:2002JAN18

<400> 131
Asp Gly Ala Leu Pro Ser Phe Leu His Pro Gln Tyr Phe Lys Tyr
1 5 10 15
Glu Phe Pro Glu Gly Val Asp Ser Val Ile Val Lys Val Thr Ser
20 25 30
Asn Lys Ala Phe Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu
35 40 45
Cys Pro Val Tyr Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met
50 55 60
Tyr Gln Thr Met Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys
65 70 75
Asp Phe Pro Ser Asn Ser Phe Tyr Val Val Val Val Val Lys Thr
80 85 90
Glu Asp Gln Ala Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala
95 100 105
Glu Asp Glu Pro Val Asp Gln Gly His Arg Gln Lys Thr Leu Ser
110 115 120
Val Leu Val Ser Gln Ala Val Thr Ser Glu Ala Tyr Val Ser Gly
125 130 135
Met Leu Phe Cys Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr
140 145 150
Val Leu Leu Ala Cys Trp Glu Asn Trp Arg Gln Lys Lys Lys Thr
155 160 165
Leu Leu Val Ala Ile Asp Arg Ala Cys Pro Glu Ser Gly His Pro
170 175 180
Arg Val Leu Ala Asp Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly
185 190 195
Tyr Asn Tyr Gly Ser Phe Glu Asn Val Ser Gly Ser Thr Asp Gly
200 205 210
Leu Val Asp Ser Ala Gly Thr Gly Asp Leu Ser Tyr Gly Tyr Gln
215 220 225
Gly His Asp Gln Phe Lys Arg Arg Leu Pro Ser Gly Gln Met Arg
230 235 240
Gln Leu Cys Ile Ala Met Gly Arg Ser Phe Glu Pro Val Gly Thr
245 250 255
Arg Pro Arg Val Asp Ser Met Ser Ser Val Glu Glu Asp Asp Tyr
260 265 270
Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn Val Ile Arg Thr
275 280 285
Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala Arg Lys Asp Lys Arg
290 295 300
Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile Ala Thr
305 310 315
Ile Ala Val Phe Tyr Ala Leu Pro Val Val Gln Leu Val Ile Thr
320 325 330
Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr
335 340 345
Tyr Asn Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala Phe
350 355 360
Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu
365 370 375

Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala
380 385 390
Leu Leu Arg Asn Asp Leu Cys Ala Leu Glu Cys Gly Ile Pro Lys
395 400 405
His Phe Gly Leu Phe Tyr Ala Met Gly Thr Ala Leu Met Met Glu
410 415 420
Gly Leu Leu Ser Ala Cys Tyr His Val Cys Pro Asn Tyr Thr Asn
425 430 435
Phe Gln Phe Asp Thr Ser Phe Met Tyr Met Ile Ala Gly Leu Cys
440 445 450
Met Leu Lys Leu Tyr Gln Lys Arg His Pro Asp Ile Asn Ala Ser
455 460 465
Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile Val Ile Phe Phe Ser
470 475 480
Val Leu Gly Val Val Phe Gly Lys Gly Asn Thr Ala Phe Trp Ile
485 490 495
Val Phe Ser Ile Ile His Ile Ile Ala Thr Leu Leu Leu Ser Thr
500 505 510
Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp Ser Gly Ile Phe
515 520 525
Arg Arg Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln Cys
530 535 540
Ser Gly Pro Leu Tyr Val Asp Arg Met Val Leu Leu Val Met Gly
545 550 555
Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg
560 565 570
Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn
575 580 585
Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg Ser
590 595 600
Gly Glu Arg Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr
605 610 615
Ser Val Val Trp Gly Phe Ala Leu Phe Phe Phe Phe Gln Gly Leu
620 625 630
Ser Thr Trp Gln Lys Thr Pro Ala Glu Ser Arg Glu His Asn Arg
635 640 645
Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp His Asp Ile Trp His
650 655 660
Phe Leu Ser Ser Ile Ala Met Phe Gly Ser Phe Leu Val Ser Gly
665 670 675
Pro Pro Gly Arg Ala Gly Trp Val Arg Glu Gly Ser Ser Cys Leu
680 685 690
Leu Leu Cys Gly

<210> 132
<211> 401
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:1347461.28.orf3:2002JAN18

<400> 132
Phe Ile Trp His Lys Ser Ile Leu Ser Arg Met Ala Glu Ala Val
1 5 10 15
Leu Ile Asp Leu Phe Gly Leu Lys Leu Asn Ser Gln Lys Asn Cys
20 25 30
His Gln Thr Leu Leu Lys Thr Leu Asn Ala Val Gln Tyr His His
35 40 45
Ala Ala Lys Ala Lys Phe Leu Cys Ile Met Cys Cys Ser Asn Ile
50 55 60

Ser Tyr Glu Arg Asp Gly Glu Gln Asp Asn Cys Glu Ile Glu Thr
65 70 75
Ser Asn Gly Leu Ser Ala Leu Leu Glu Glu Phe Glu Ile Val Ser
80 85 90
Cys Pro Ser Met Ala Ala Thr Leu Tyr Thr Ile Lys Gln Lys Ile
95 100 105
Asp Glu Lys Asn Leu Ser Ser Ile Lys Val Ile Val Pro Arg His
110 115 120
Arg Lys Thr Leu Met Lys Ala Phe Ile Asp Gln Leu Phe Thr Asp
125 130 135
Val Tyr Asn Phe Glu Phe Glu Asp Leu Gln Val Thr Phe Arg Gly
140 145 150
Gly Leu Phe Lys Gln Ser Ile Glu Ile Asn Val Ile Thr Ala Gln
155 160 165
Glu Leu Arg Gly Ile Gln Asn Glu Ile Glu Thr Phe Leu Arg Ser
170 175 180
Leu Pro Ala Leu Arg Gly Lys Leu Thr Ile Ile Thr Ser Ser Leu
185 190 195
Ile Pro Asp Ile Phe Ile His Gly Phe Thr Thr Arg Thr Gly Gly
200 205 210
Ile Ser Tyr Ile Pro Thr Leu Ser Ser Phe Asn Leu Phe Ser Ser
215 220 225
Ser Lys Arg Arg Asp Pro Lys Val Val Val Gln Gly Ile Lys Thr
230 235 240
His His Ser Asn Asp Ile Trp Ile Met Gly Arg Lys Glu Pro Asp
245 250 255
Ser Tyr Asp Gly Ile Thr Thr Asn Gln Arg Gly Val Thr Ile Ala
260 265 270
Ala Leu Gly Ala Asp Cys Ile Pro Ile Val Phe Ala Asp Pro Val
275 280 285
Lys Lys Ala Cys Gly Val Ala His Ala Gly Trp Lys Gly Thr Leu
290 295 300
Leu Gly Val Ala Met Ala Thr Val Asn Ala Met Ile Ala Glu Tyr
305 310 315
Gly Cys Ser Leu Glu Asp Ile Val Val Val Leu Gly Pro Ser Val
320 325 330
Gly Pro Cys Cys Phe Thr Leu Pro Arg Glu Ser Ala Glu Ala Phe
335 340 345
His Asn Leu His Pro Ala Cys Val Gln Leu Phe Asp Ser Pro Asn
350 355 360
Pro Cys Ile Asp Ile Arg Lys Ala Thr Ser Phe Pro Lys Asp Ser
365 370 375
Ser Arg Thr Gly Arg Asn Ser Ser Thr Glu Tyr Ser Gly Pro Glu
380 385 390
Pro Arg Ser Gln Pro Leu Tyr Ile Leu Pro Ser
395 400

<210> 133
<211> 141
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:1383494.16.orf3:2002JAN18

<400> 133
Ser Gln His Phe Pro Arg Pro Ser Val Glu Thr Glu Val Gly Asp
1 5 10 15
Tyr Met Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys
20 25 30
Val Ile Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala
35 40 45

Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile
50 55 60
Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile Asn Ser Ile
65 70 75
Lys Ser Arg Leu Ser Lys Ser Gly His Ile Gln Thr Leu Leu Arg
80 85 90
Ala Phe Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp
95 100 105
Arg Val Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val
110 115 120
Val Ser Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp
125 130 135
Lys Arg Lys Ser Arg Thr
140

<210> 134
<211> 340
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:1400155.1.orf2:2002JAN18

<400> 134
Ala Trp Ala Ala Val Ile Thr Pro Trp Asn Phe Pro Ser Ala Met
1 5 10 15
Ile Thr Arg Lys Val Gly Ala Ala Leu Ala Ala Gly Cys Thr Val
20 25 30
Val Val Lys Pro Ala Glu Asp Thr Pro Phe Ser Ala Leu Ala Leu
35 40 45
Ala Glu Leu Ala Ser Gln Ala Gly Ile Pro Ser Gly Val Tyr Asn
50 55 60
Val Ile Pro Cys Ser Arg Lys Asn Ala Lys Glu Val Gly Glu Ala
65 70 75
Ile Cys Thr Asp Pro Leu Val Ser Lys Ile Ser Phe Thr Gly Ser
80 85 90
Thr Thr Thr Gly Lys Ile Leu Leu His His Ala Ala Asn Ser Val
95 100 105
Lys Arg Val Ser Met Glu Leu Gly Gly Leu Ala Pro Phe Ile Val
110 115 120
Phe Asp Ser Ala Asn Val Asp Gln Ala Val Ala Gly Ala Met Ala
125 130 135
Ser Lys Phe Arg Asn Thr Gly Gln Thr Cys Val Cys Ser Asn Gln
140 145 150
Phe Leu Val Gln Arg Gly Ile His Asp Ala Phe Val Lys Ala Phe
155 160 165
Ala Glu Ala Met Lys Lys Asn Leu Arg Val Gly Asn Gly Phe Glu
170 175 180
Glu Gly Thr Thr Gln Gly Pro Leu Ile Asn Glu Lys Ala Val Glu
185 190 195
Lys Val Glu Lys Gln Val Asn Asp Ala Val Ser Lys Gly Ala Thr
200 205 210
Val Val Thr Gly Gly Lys Arg His Gln Leu Gly Lys Asn Phe Phe
215 220 225
Glu Pro Thr Leu Leu Cys Asn Val Thr Gln Asp Met Leu Cys Thr
230 235 240
His Glu Glu Thr Phe Gly Pro Leu Ala Pro Val Ile Lys Phe Asp
245 250 255
Thr Glu Glu Glu Ala Ile Ala Ile Ala Asn Ala Ala Asp Val Gly
260 265 270
Leu Ala Gly Tyr Phe Tyr Ser Gln Asp Pro Ala Gln Ile Trp Arg
275 280 285

Val Ala Glu Gln Leu Glu Val Gly Met Val Gly Val Asn Glu Gly
290 295 300
Leu Ile Ser Ser Val Glu Cys Pro Phe Gly Gly Val Lys Gln Ser
305 310 315
Gly Leu Gly Arg Glu Gly Ser Lys Tyr Gly Ile Asp Glu Tyr Leu
320 325 330
Glu Leu Lys Tyr Val Cys Tyr Gly Gly Leu
335 340

<210> 135
<211> 229
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:1446621.1.orf3:2002JAN18

<400> 135
Lys Leu Asp Tyr Arg Arg Glu Pro Pro Arg Pro Val Tyr Val Leu
1 5 10 15
Trp Ile Cys Glu Tyr Ser Tyr Ser Val Leu Phe Ile Asn Thr Tyr
20 25 30
Asp Leu Thr Gln Lys Val Lys Val Asn Thr Leu Trp Gly Gly Pro
35 40 45
Val Ser Val Gln Gly Gly Ser Pro Ala Arg Lys Gly Cys Ser Leu
50 55 60
Arg Cys His Ser Ser Phe Ser Pro Ala Ser Asp His Ile Cys His
65 70 75
Ser Gly Pro Glu Gly Ala Gly Gly Pro Ser Asn Gln Ala Arg Ser
80 85 90
Trp Ser Arg Gln Gly Gly Phe Arg Gly Phe Gly Ala Ala Phe Val
95 100 105
Ser Arg Cys Arg Gln Lys Leu Gln Phe Ser Ser Val Cys Phe Val
110 115 120
Ser Ser Ala Arg Arg Ser Pro Ala Cys Val Ala Leu Arg Pro Ala
125 130 135
Gly Ile Gly Arg Ser Thr Ala Lys Thr Pro Gly Pro Pro Gly Ser
140 145 150
Leu Glu Met Gly Ala Leu Thr Phe Arg Asp Val Ala Ile Glu Phe
155 160 165
Ser Leu Glu Glu Trp Gln Cys Leu Asp Thr Glu Gln Gln Asn Leu
170 175 180
Tyr Arg Asn Val Met Leu Asp Asn Tyr Arg Asn Leu Val Phe Leu
185 190 195
Gly Ile Ala Val Ser Lys Pro Asp Leu Ile Thr Cys Leu Glu Gln
200 205 210
Glu Lys Glu Pro Trp Asn Leu Lys Thr His Asp Met Val Ala Lys
215 220 225
Pro Pro Gly Arg

<210> 136
<211> 407
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:144920.1.orf1:2002JAN18

<400> 136
Val Leu Leu Asp Glu Ala Gln Arg Leu Leu Tyr Arg Asp Val Met

1 5 10 15
Leu Glu Asn Phe Ala Leu Met Ala Ser Leu Gly Cys Trp His Gly
20 25 30
Met Glu Asp Glu Glu Ile Pro Phe Glu Gln Ser Phe Ser Ile Gly
35 40 45
Met Ser Gln Ile Arg Ile Pro Lys Gly Gly Pro Ser Thr Gln Lys
50 55 60
Ala Tyr Pro Cys Gly Thr Cys Gly Leu Val Leu Lys Asp Ile Leu
65 70 75
His Leu Ala Glu His Gln Glu Thr His Pro Gly Gln Lys Pro Tyr
80 85 90
Met Cys Val Leu Cys Gly Lys Gln Phe Trp Phe Ser Ala Asn Leu
95 100 105
His Gln His Gln Lys Gln His Ser Gly Glu Lys Pro Phe Arg Ser
110 115 120
Asp Lys Ser Arg Pro Phe Leu Leu Asn Asn Cys Ala Val Gln Ser
125 130 135
Leu Glu Met Ser Phe Val Thr Gly Glu Ala Cys Lys Asp Phe Leu
140 145 150
Ala Ser Ser Ser Ile Phe Glu His His Ala Pro His Asn Glu Trp
155 160 165
Lys Pro His Ser Asn Thr Lys Cys Glu Glu Ala Ser His Cys Gly
170 175 180
Lys Arg His Tyr Lys Cys Ser Glu Cys Gly Lys Thr Phe Ser Arg
185 190 195
Lys Asp Ser Leu Val Gln His Gln Arg Val His Thr Gly Glu Arg
200 205 210
Pro Tyr Glu Cys Gly Glu Cys Gly Lys Thr Phe Ser Arg Lys Pro
215 220 225
Ile Leu Ala Gln His Gln Arg Ile His Thr Gly Glu Met Pro Tyr
230 235 240
Glu Cys Gly Ile Cys Gly Lys Val Phe Asn His Ser Ser Asn Leu
245 250 255
Ile Val His Gln Arg Val His Thr Gly Ala Arg Pro Tyr Lys Cys
260 265 270
Ser Glu Cys Gly Lys Ala Tyr Ser His Lys Ser Thr Leu Val Gln
275 280 285
His Glu Ser Ile His Thr Gly Glu Arg Pro Tyr Glu Cys Ser Glu
290 295 300
Cys Gly Lys Tyr Phe Gly His Lys Tyr Arg Leu Ile Lys His Trp
305 310 315
Ser Val His Thr Gly Ala Arg Pro Tyr Glu Cys Ile Ala Cys Gly
320 325 330
Lys Phe Phe Ser Gln Ser Ser Asp Leu Ile Ala His Gln Arg Val
335 340 345
His Asn Gly Glu Lys Pro Tyr Val Cys Ser Glu Cys Gly Lys Ala
350 355 360
Phe Ser His Lys His Val Leu Val Gln His His Arg Ile His Thr
365 370 375
Gly Glu Arg Pro Tyr Lys Cys Ser Glu Cys Gly Lys Ala Phe Arg
380 385 390
Gln Arg Ala Ser Leu Ile Arg His Trp Lys Ile His Thr Gly Glu
395 400 405
Arg Pro

<210> 137
<211> 529
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature

<223> Incyte ID No: LG:1452619.1.orf2:2002JAN18

<400> 137
Arg Gln Gln Leu Arg Gln Arg Gln Ala Gln Val Gln Pro Leu Ala
1 5 10 15
Glu His Asn Phe Phe Phe Ser Lys Phe Pro Gly Cys Gly Glu Leu
20 25 30
Ser Leu Gly Glu Val Lys Ser Leu Ser Ser Lys Lys Met Asn Gly
35 40 45
Thr Leu Asp His Pro Asp Gln Pro Asp Leu Asp Ala Ile Lys Met
50 55 60
Phe Val Gly Gln Val Pro Arg Thr Trp Ser Glu Lys Asp Leu Arg
65 70 75
Glu Leu Phe Glu Gln Tyr Gly Ala Val Tyr Glu Ile Asn Val Leu
80 85 90
Arg Asp Arg Ser Gln Asn Pro Pro Gln Ser Lys Gly Cys Cys Phe
95 100 105
Val Thr Phe Tyr Thr Arg Lys Ala Ala Leu Glu Ala Gln Asn Ala
110 115 120
Leu His Asn Met Lys Val Leu Pro Gly Met His His Pro Ile Gln
125 130 135
Met Lys Pro Ala Asp Ser Glu Lys Asn Asn Ala Val Glu Asp Arg
140 145 150
Lys Leu Phe Ile Gly Met Ile Ser Lys Lys Cys Thr Glu Asn Asp
155 160 165
Ile Arg Val Met Phe Ser Ser Phe Gly Gln Ile Glu Glu Cys Arg
170 175 180
Ile Leu Arg Gly Pro Asp Gly Leu Ser Arg Gly Cys Ala Phe Val
185 190 195
Thr Phe Thr Thr Arg Ala Met Ala Gln Thr Ala Ile Lys Ala Met
200 205 210
His Gln Ala Gln Thr Met Glu Gly Cys Ser Ser Pro Met Val Val
215 220 225
Lys Phe Ala Asp Thr Gln Lys Asp Lys Glu Gln Lys Arg Met Ala
230 235 240
Gln Gln Leu Gln Gln Gln Met Gln Gln Ile Ser Ala Ala Ser Val
245 250 255
Trp Gly Asn Leu Ala Gly Leu Asn Thr Leu Gly Pro Gln Tyr Leu
260 265 270
Ala Leu Tyr Leu Gln Leu Leu Gln Gln Thr Ala Ser Ser Gly Asn
275 280 285
Leu Asn Thr Leu Ser Ser Leu His Pro Met Gly Gly Leu Asn Ala
290 295 300
Met Gln Leu Gln Asn Leu Ala Ala Leu Ala Ala Ala Ala Ser Ala
305 310 315
Ala Gln Asn Thr Pro Ser Gly Thr Asn Ala Leu Thr Thr Ser Ser
320 325 330
Ser Pro Leu Ser Val Leu Thr Ser Ser Ala Gly Ser Ser Pro Ser
335 340 345
Ser Ser Ser Ser Asn Ser Val Asn Pro Ile Ala Ser Leu Gly Ala
350 355 360
Leu Gln Thr Leu Ala Gly Ala Thr Ala Gly Leu Asn Val Gly Ser
365 370 375
Leu Ala Gly Met Ala Ala Leu Asn Gly Gly Leu Gly Ser Ser Gly
380 385 390
Leu Ser Asn Gly Thr Gly Ser Thr Met Glu Ala Leu Thr Gln Ala
395 400 405
Tyr Ser Gly Ile Gln Gln Tyr Ala Ala Ala Ala Leu Pro Thr Leu
410 415 420
Tyr Asn Gln Asn Leu Leu Thr Gln Gln Ser Ile Gly Ala Ala Gly
425 430 435
Ser Gln Lys Glu Gly Pro Glu Gly Ala Asn Leu Phe Ile Tyr His
440 445 450

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Leu Pro Gln Glu Phe Gly Asp Gln Asp Leu Leu Gln Met Phe Met
                455                 460                 465
Pro Phe Gly Asn Val Val Ser Ala Lys Val Phe Ile Asp Lys Gln
                470                 475                 480
Thr Asn Leu Ser Lys Cys Phe Gly Phe Val Ser Tyr Asp Asn Pro
                485                 490                 495
Val Ser Ala Gln Ala Ala Ile Gln Ser Met Asn Gly Phe Gln Ile
                500                 505                 510
Gly Met Lys Arg Leu Lys Val Gln Leu Lys Arg Ser Lys Asn Asp
                515                 520                 525
Ser Lys Pro Tyr
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<210> 138
<211> 2245
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:1453417.6.orf1:2002JAN18

<400> 138
Ala Ala Val Cys Val Gly Cys Tyr Arg Leu Arg Trp His Ser Ala
1               5                   10                  15
Gly His Gly Thr Asp Cys Gly Glu Cys His Arg Arg His Thr His
                20                  25                  30
Arg Pro Val Phe Gln Ser Ser His Tyr Thr Val Asn Val Asn Glu
                35                  40                  45
Asp Arg Pro Ala Gly Thr Thr Val Val Leu Ile Ser Ala Thr Asp
                50                  55                  60
Glu Asp Thr Gly Glu Asn Ala Arg Ile Thr Tyr Phe Met Glu Asp
                65                  70                  75
Ser Ile Pro Gln Phe Arg Ile Asp Ala Asp Thr Gly Ala Val Thr
                80                  85                  90
Thr Gln Ala Glu Leu Asp Tyr Glu Asp Gln Val Ser Tyr Thr Leu
                95                  100                 105
Ala Ile Thr Ala Arg Asp Asn Gly Ile Pro Gln Lys Ser Asp Thr
                110                 115                 120
Thr Tyr Leu Glu Ile Leu Val Asn Asp Val Asn Asp Asn Ala Pro
                125                 130                 135
Gln Phe Leu Arg Asp Ser Tyr Gln Gly Ser Val Tyr Glu Asp Val
                140                 145                 150
Pro Pro Phe Thr Ser Val Leu Gln Ile Ser Ala Thr Asp Arg Asp
                155                 160                 165
Ser Gly Leu Asn Gly Arg Val Phe Tyr Thr Phe Gln Gly Gly Asp
                170                 175                 180
Asp Gly Asp Gly Asp Phe Ile Val Glu Ser Thr Ser Gly Ile Val
                185                 190                 195
Arg Thr Leu Arg Arg Leu Asp Arg Glu Asn Val Ala Gln Tyr Val
                200                 205                 210
Leu Arg Ala Tyr Ala Val Asp Lys Gly Met Pro Pro Ala Arg Thr
                215                 220                 225
Pro Met Glu Val Thr Val Thr Val Leu Asp Val Asn Asp Asn Pro
                230                 235                 240
Pro Val Phe Glu Gln Asp Glu Phe Asp Val Phe Val Glu Glu Asn
                245                 250                 255
Ser Pro Ile Gly Leu Ala Val Ala Arg Val Thr Ala Thr Asp Pro
                260                 265                 270
Asp Glu Gly Thr Asn Ala Gln Ile Met Tyr Gln Ile Val Glu Gly
                275                 280                 285
Asn Ile Pro Glu Val Phe Gln Leu Asp Ile Phe Ser Gly Glu Leu
                290                 295                 300
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Thr Ala Leu Val Asp Leu Asp Tyr Glu Asp Arg Pro Glu Tyr Val
305 310 315
Leu Val Ile Gln Ala Thr Ser Ala Pro Leu Val Ser Arg Ala Thr
320 325 330
Val His Val Arg Leu Leu Asp Arg Asn Asp Asn Pro Pro Val Leu
335 340 345
Gly Asn Phe Glu Ile Leu Phe Asn Asn Tyr Val Thr Asn Arg Ser
350 355 360
Ser Ser Phe Pro Gly Gly Ala Ile Gly Arg Val Pro Ala His Asp
365 370 375
Pro Asp Ile Ser Asp Ser Leu Thr Tyr Ser Phe Glu Arg Gly Asn
380 385 390
Glu Leu Ser Leu Val Leu Leu Asn Ala Ser Thr Gly Glu Leu Lys
395 400 405
Leu Ser Arg Ala Leu Asp Asn Asn Arg Pro Leu Glu Ala Ile Met
410 415 420
Ser Val Leu Val Ser Asp Gly Val His Ser Val Thr Ala Gln Cys
425 430 435
Ala Leu Arg Val Thr Ile Ile Thr Asp Glu Met Leu Thr His Ser
440 445 450
Ile Thr Leu Arg Leu Glu Asp Met Ser Pro Glu Arg Phe Leu Ser
455 460 465
Pro Leu Leu Gly Leu Phe Ile Gln Ala Val Ala Ala Thr Leu Ala
470 475 480
Thr Pro Pro Asp His Val Val Val Phe Asn Val Gln Arg Asp Thr
485 490 495
Asp Ala Pro Gly Gly His Ile Leu Asn Val Ser Leu Ser Val Gly
500 505 510
Gln Pro Pro Gly Pro Gly Gly Gly Pro Pro Phe Leu Pro Ser Glu
515 520 525
Asp Leu Gln Glu Arg Leu Tyr Leu Asn Arg Ser Leu Leu Thr Ala
530 535 540
Ile Ser Ala Gln Arg Val Leu Pro Phe Asp Asp Asn Ile Cys Leu
545 550 555
Arg Glu Pro Cys Glu Asn Tyr Met Arg Cys Val Ser Val Leu Arg
560 565 570
Phe Asp Ser Ser Ala Pro Phe Ile Ala Ser Ser Ser Val Leu Phe
575 580 585
Arg Pro Ile His Pro Val Gly Gly Leu Arg Cys Arg Cys Pro Pro
590 595 600
Gly Phe Thr Gly Asp Tyr Cys Glu Thr Glu Val Asp Leu Cys Tyr
605 610 615
Ser Arg Pro Cys Gly Pro His Gly Arg Cys Arg Ser Arg Glu Gly
620 625 630
Gly Tyr Thr Cys Leu Cys Arg Asp Gly Tyr Thr Gly Glu His Cys
635 640 645
Glu Val Ser Ala Arg Ser Gly Arg Cys Thr Pro Gly Val Cys Lys
650 655 660
Asn Gly Gly Thr Cys Val Asn Leu Leu Val Gly Gly Phe Lys Cys
665 670 675
Asp Cys Pro Ser Gly Asp Phe Glu Lys Pro Tyr Cys Gln Val Thr
680 685 690
Thr Arg Ser Phe Pro Ala His Ser Phe Ile Thr Phe Arg Gly Leu
695 700 705
Arg Gln Arg Phe His Phe Thr Leu Ala Leu Ser Phe Ala Thr Lys
710 715 720
Glu Arg Asp Gly Leu Leu Leu Tyr Asn Gly Arg Phe Asn Glu Lys
725 730 735
His Asp Phe Val Ala Leu Glu Val Ile Gln Glu Gln Val Gln Leu
740 745 750
Thr Phe Ser Ala Gly Glu Ser Thr Thr Thr Val Ser Pro Phe Val
755 760 765
Pro Gly Gly Val Ser Asp Gly Gln Trp His Thr Val Gln Leu Lys

770 775 780
Tyr Tyr Asn Lys Pro Leu Leu Gly Gln Thr Gly Leu Pro Gln Gly
785 790 795
Pro Ser Glu Gln Lys Val Ala Val Val Thr Val Asp Gly Cys Asp
800 805 810
Thr Gly Val Ala Leu Arg Phe Gly Ser Val Leu Gly Asn Tyr Ser
815 820 825
Cys Ala Ala Gln Gly Thr Gln Gly Gly Ser Lys Lys Ser Leu Asp
830 835 840
Leu Thr Gly Pro Leu Leu Leu Gly Gly Val Pro Asp Leu Pro Glu
845 850 855
Ser Phe Pro Val Arg Met Arg Gln Phe Val Gly Cys Met Arg Asn
860 865 870
Leu Gln Val Asp Ser Arg His Ile Asp Met Ala Asp Phe Ile Ala
875 880 885
Asn Asn Gly Thr Val Pro Gly Cys Pro Ala Lys Lys Asn Val Cys
890 895 900
Asp Ser Asn Thr Cys His Asn Gly Gly Thr Cys Val Asn Gln Trp
905 910 915
Asp Ala Phe Ser Cys Glu Cys Pro Leu Gly Phe Gly Gly Lys Ser
920 925 930
Cys Ala Gln Glu Met Ala Asn Pro Gln His Phe Leu Gly Ser Ser
935 940 945
Leu Val Ala Trp His Gly Leu Ser Leu Pro Ile Ser Gln Pro Trp
950 955 960
Tyr Leu Ser Leu Met Phe Arg Thr Arg Gln Ala Asp Gly Val Leu
965 970 975
Leu Gln Ala Ile Thr Arg Gly Arg Ser Thr Ile Thr Leu Gln Leu
980 985 990
Arg Glu Gly His Val Met Leu Ser Val Glu Gly Thr Gly Leu Gln
995 1000 1005
Ala Ser Ser Leu Arg Leu Glu Pro Gly Arg Ala Asn Asp Gly Asp
1010 1015 1020
Trp His His Ala Gln Leu Ala Leu Gly Ala Ser Gly Gly Pro Gly
1025 1030 1035
His Ala Ile Leu Ser Phe Asp Tyr Gly Gln Gln Arg Ala Glu Gly
1040 1045 1050
Asn Leu Gly Pro Arg Leu His Gly Leu His Leu Ser Asn Ile Thr
1055 1060 1065
Val Gly Gly Ile Pro Gly Pro Ala Gly Gly Val Ala Arg Gly Phe
1070 1075 1080
Arg Gly Cys Leu Gln Gly Val Arg Val Ser Asp Thr Pro Glu Gly
1085 1090 1095
Val Asn Ser Leu Asp Pro Ser His Gly Glu Ser Ile Asn Val Glu
1100 1105 1110
Gln Gly Cys Ser Leu Pro Asp Pro Cys Asp Ser Asn Pro Cys Pro
1115 1120 1125
Ala Asn Ser Tyr Cys Ser Asn Asp Trp Asp Ser Tyr Ser Cys Ser
1130 1135 1140
Cys Asp Pro Gly Tyr Tyr Gly Asp Asn Cys Thr Asn Val Cys Asp
1145 1150 1155
Leu Asn Pro Cys Glu His Gln Ser Val Cys Thr Arg Lys Pro Ser
1160 1165 1170
Ala Pro His Gly Tyr Thr Cys Glu Cys Pro Pro Asn Tyr Leu Gly
1175 1180 1185
Pro Tyr Cys Glu Thr Arg Ile Asp Gln Pro Cys Pro Arg Gly Trp
1190 1195 1200
Trp Gly His Pro Thr Cys Gly Pro Cys Asn Cys Asp Val Ser Lys
1205 1210 1215
Gly Phe Asp Pro Asp Cys Asn Lys Thr Ser Gly Glu Cys His Cys
1220 1225 1230
Lys Glu Asn His Tyr Arg Pro Pro Gly Ser Pro Thr Cys Leu Leu
1235 1240 1245

Cys Asp Cys Tyr Pro Thr Gly Ser Leu Ser Arg Val Cys Asp Pro
1250 1255 1260
Glu Asp Gly Gln Cys Pro Cys Lys Pro Gly Val Ile Gly Arg Gln
1265 1270 1275
Cys Asp Arg Cys Asp Asn Pro Phe Ala Glu Val Thr Thr Asn Gly
1280 1285 1290
Cys Glu Val Asn Tyr Asp Ser Cys Pro Arg Ala Ile Glu Ala Gly
1295 1300 1305
Ile Trp Trp Pro Arg Thr Arg Phe Gly Leu Pro Ala Ala Ala Pro
1310 1315 1320
Cys Pro Lys Gly Ser Phe Gly Thr Ala Val Arg His Cys Asp Glu
1325 1330 1335
His Arg Gly Trp Leu Pro Pro Asn Leu Phe Asn Cys Thr Ser Ile
1340 1345 1350
Thr Phe Ser Glu Leu Lys Gly Phe Ala Glu Arg Leu Gln Arg Asn
1355 1360 1365
Glu Ser Gly Leu Asp Ser Gly Arg Ser Gln Gln Leu Ala Leu Leu
1370 1375 1380
Leu Arg Asn Ala Thr Gln His Thr Ala Gly Tyr Phe Gly Ser Asp
1385 1390 1395
Val Lys Val Ala Tyr Gln Leu Ala Thr Arg Leu Leu Ala His Glu
1400 1405 1410
Ser Thr Gln Arg Gly Phe Gly Leu Ser Ala Thr Gln Asp Val His
1415 1420 1425
Phe Thr Glu Asn Leu Leu Arg Val Gly Ser Ala Leu Leu Asp Thr
1430 1435 1440
Ala Asn Lys Arg His Trp Glu Leu Ile Gln Gln Thr Glu Gly Gly
1445 1450 1455
Thr Ala Trp Leu Leu Gln His Tyr Glu Ala Tyr Ala Ser Ala Leu
1460 1465 1470
Ala Gln Asn Met Arg His Thr Tyr Leu Ser Pro Phe Thr Ile Val
1475 1480 1485
Thr Pro Asn Ile Val Ile Ser Val Val Arg Leu Asp Lys Gly Asn
1490 1495 1500
Phe Ala Gly Ala Lys Leu Pro Arg Tyr Glu Ala Leu Arg Gly Glu
1505 1510 1515
Gln Pro Pro Asp Leu Glu Thr Thr Val Ile Leu Pro Glu Ser Val
1520 1525 1530
Phe Arg Glu Thr Pro Pro Val Val Arg Pro Ala Gly Pro Gly Glu
1535 1540 1545
Ala Gln Glu Pro Glu Glu Leu Ala Arg Arg Gln Arg Arg His Pro
1550 1555 1560
Glu Leu Ser Gln Gly Glu Ala Val Ala Ser Val Ile Ile Tyr Arg
1565 1570 1575
Thr Leu Ala Gly Leu Leu Pro His Asn Tyr Asp Pro Asp Lys Arg
1580 1585 1590
Ser Leu Arg Val Pro Lys Arg Pro Ile Ile Asn Thr Pro Val Val
1595 1600 1605
Ser Ile Ser Val His Asp Asp Glu Glu Leu Leu Pro Arg Ala Leu
1610 1615 1620
Asp Lys Pro Val Thr Val Gln Phe Arg Leu Leu Glu Thr Glu Glu
1625 1630 1635
Arg Thr Lys Pro Ile Cys Val Phe Trp Asn His Ser Ile Leu Val
1640 1645 1650
Ser Gly Thr Gly Gly Trp Ser Ala Arg Gly Cys Glu Val Val Phe
1655 1660 1665
Arg Asn Glu Ser His Val Ser Cys Gln Cys Asn His Met Thr Ser
1670 1675 1680
Phe Ala Val Leu Met Asp Val Ser Arg Arg Glu Asn Gly Glu Ile
1685 1690 1695
Leu Pro Leu Lys Thr Leu Thr Tyr Val Ala Leu Gly Val Thr Leu
1700 1705 1710
Ala Ala Leu Leu Leu Thr Phe Phe Phe Leu Thr Leu Leu Arg Ile

1715 1720 1725
Leu Arg Ser Asn Gln His Gly Ile Arg Arg Asn Leu Thr Ala Ala
1730 1735 1740
Leu Gly Leu Ala Gln Leu Val Phe Leu Leu Gly Ile Asn Gln Ala
1745 1750 1755
Asp Leu Pro Phe Ala Cys Thr Val Ile Ala Ile Leu Leu His Phe
1760 1765 1770
Leu Tyr Leu Cys Thr Phe Ser Trp Ala Leu Leu Glu Ala Leu His
1775 1780 1785
Leu Tyr Arg Ala Leu Thr Glu Val Arg Asp Val Asn Thr Gly Pro
1790 1795 1800
Met Arg Phe Tyr Tyr Met Leu Gly Trp Gly Val Pro Ala Phe Ile
1805 1810 1815
Thr Gly Leu Ala Val Gly Leu Asp Pro Glu Gly Tyr Gly Asn Pro
1820 1825 1830
Asp Phe Cys Trp Leu Ser Ile Tyr Asp Thr Leu Ile Trp Ser Phe
1835 1840 1845
Ala Gly Pro Val Ala Phe Ala Val Ser Met Ser Val Phe Leu Tyr
1850 1855 1860
Ile Leu Ala Ala Arg Ala Ser Cys Ala Ala Gln Arg Gln Gly Phe
1865 1870 1875
Glu Lys Lys Gly Pro Val Ser Gly Leu Gln Pro Ser Phe Ala Val
1880 1885 1890
Leu Leu Leu Leu Ser Ala Thr Trp Leu Leu Ala Leu Leu Ser Val
1895 1900 1905
Asn Ser Asp Thr Leu Leu Phe His Tyr Leu Phe Ala Thr Cys Asn
1910 1915 1920
Cys Ile Gln Gly Pro Phe Ile Phe Leu Ser Tyr Val Val Leu Ser
1925 1930 1935
Lys Glu Val Arg Lys Ala Leu Lys Leu Ala Cys Ser Arg Lys Pro
1940 1945 1950
Ser Pro Asp Pro Ala Leu Thr Thr Lys Ser Thr Leu Thr Ser Ser
1955 1960 1965
Tyr Asn Cys Pro Ser Pro Tyr Ala Asp Gly Arg Leu Tyr Gln Pro
1970 1975 1980
Tyr Gly Asp Ser Ala Gly Ser Leu His Ser Thr Ser Arg Ser Gly
1985 1990 1995
Lys Ser Gln Pro Ser Tyr Ile Pro Phe Leu Leu Arg Glu Glu Ser
2000 2005 2010
Ala Leu Asn Pro Gly Gln Gly Pro Pro Gly Leu Gly Asp Pro Gly
2015 2020 2025
Ser Leu Phe Leu Glu Gly Gln Asp Gln Gln His Asp Pro Asp Thr
2030 2035 2040
Asp Ser Asp Ser Asp Leu Ser Leu Glu Asp Asp Gln Ser Gly Ser
2045 2050 2055
Tyr Ala Ser Thr His Ser Ser Asp Ser Glu Glu Glu Glu Glu Glu
2060 2065 2070
Glu Glu Glu Glu Ala Ala Phe Pro Gly Glu Gln Gly Trp Asp Ser
2075 2080 2085
Leu Leu Gly Pro Gly Ala Glu Arg Leu Pro Leu His Ser Thr Pro
2090 2095 2100
Lys Asp Gly Gly Pro Gly Pro Gly Lys Ala Pro Trp Pro Gly Asp
2105 2110 2115
Phe Gly Thr Thr Ala Lys Glu Ser Ser Gly Asn Gly Ala Pro Glu
2120 2125 2130
Glu Arg Leu Arg Glu Asn Gly Asp Ala Leu Ser Arg Glu Gly Ser
2135 2140 2145
Leu Gly Pro Leu Pro Gly Ser Ser Ala Gln Pro His Lys Gly Ile
2150 2155 2160
Leu Lys Lys Lys Cys Leu Pro Thr Ile Ser Glu Lys Ser Ser Leu
2165 2170 2175
Leu Arg Leu Pro Leu Glu Gln Cys Thr Gly Ser Ser Arg Gly Ser
2180 2185 2190

Ser Ala Ser Glu Gly Ser Arg Gly Gly Pro Pro Pro Arg Pro Pro
2195 2200 2205
Pro Arg Gln Ser Leu Gln Glu Gln Leu Asn Gly Val Met Pro Ile
2210 2215 2220
Ala Met Ser Ile Lys Ala Gly Thr Val Asp Glu Asp Ser Ser Gly
2225 2230 2235
Ser Glu Phe Leu Phe Phe Asn Phe Leu His
2240 2245

<210> 139
<211> 490
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:148485.8.orf1:2002JAN18

<400> 139
Ile Gly Met Ser Gly Leu Leu Thr Asp Pro Glu Gln Arg Ala Gln
1 5 10 15
Glu Pro Arg Tyr Pro Gly Phe Val Leu Gly Leu Asp Val Gly Ser
20 25 30
Ser Val Ile Arg Cys His Val Tyr Asp Arg Ala Ala Arg Val Cys
35 40 45
Gly Ser Ser Val Gln Lys Val Glu Asn Leu Tyr Pro Gln Ile Gly
50 55 60
Trp Val Glu Ile Asp Pro Asp Val Leu Trp Ile Gln Phe Val Ala
65 70 75
Val Ile Lys Glu Ala Val Lys Ala Ala Gly Ile Gln Met Asn Gln
80 85 90
Ile Val Gly Leu Gly Ile Ser Thr Gln Arg Ala Thr Phe Ile Thr
95 100 105
Trp Asn Lys Lys Thr Gly Asn His Phe His Asn Phe Ile Ser Trp
110 115 120
Gln Asp Leu Arg Ala Val Glu Leu Val Lys Ser Trp Asn Asn Ser
125 130 135
Leu Leu Met Lys Ile Phe His Ser Ser Cys Arg Val Leu His Phe
140 145 150
Phe Thr Arg Ser Lys Arg Leu Phe Thr Ala Ser Leu Phe Thr Phe
155 160 165
Thr Thr Gln Gln Thr Ser Leu Arg Leu Val Trp Ile Leu Gln Asn
170 175 180
Leu Thr Glu Val Gln Lys Ala Val Glu Glu Glu Asn Cys Cys Phe
185 190 195
Gly Thr Ile Asp Thr Trp Leu Leu Tyr Lys Leu Thr Lys Gly Ser
200 205 210
Val Tyr Ala Thr Asp Phe Ser Asn Ala Ser Thr Thr Gly Leu Phe
215 220 225
Asp Pro Tyr Lys Met Cys Trp Ser Gly Met Ile Thr Ser Leu Ile
230 235 240
Ser Ile Pro Leu Ser Leu Leu Pro Pro Val Arg Asp Thr Ser His
245 250 255
Asn Phe Gly Ser Val Asp Glu Glu Ile Phe Gly Val Pro Ile Pro
260 265 270
Ile Val Ala Leu Val Ala Asp Gln Gln Ser Ala Met Phe Gly Glu
275 280 285
Cys Cys Phe Gln Thr Gly Asp Val Lys Leu Thr Met Gly Thr Gly
290 295 300
Thr Phe Leu Asp Ile Asn Thr Gly Asn Ser Leu Gln Gln Thr Thr
305 310 315
Gly Gly Phe Tyr Pro Leu Ile Gly Trp Lys Ile Gly Gln Glu Val
320 325 330

Val Cys Leu Ala Glu Ser Asn Ala Gly Asp Thr Gly Thr Ala Ile
335 340 345
Lys Trp Ala Gln Gln Leu Asp Leu Phe Thr Asp Ala Ala Glu Thr
350 355 360
Glu Lys Met Ala Lys Ser Leu Glu Asp Ser Glu Gly Val Cys Phe
365 370 375
Val Pro Ser Phe Ser Gly Leu Gln Ala Pro Leu Asn Asp Pro Trp
380 385 390
Ala Cys Ala Ser Phe Met Gly Leu Lys Pro Ser Thr Ser Lys Tyr
395 400 405
His Leu Val Arg Ala Ile Leu Glu Ser Ile Ala Phe Arg Asn Lys
410 415 420
Gln Leu Tyr Glu Met Met Lys Lys Glu Ile His Ile Pro Val Arg
425 430 435
Lys Ile Arg Ala Asp Gly Gly Val Cys Lys Asn Gly Phe Val Met
440 445 450
Gln Met Thr Ser Asp Leu Ile Asn Glu Asn Ile Asp Arg Pro Ala
455 460 465
Asp Ile Asp Met Ser Cys Leu Gly Ala Ala Ser Leu Ala Gly Leu
470 475 480
Ala Val Gly Phe Gly Leu Thr Arg Arg Asn
485 490

<210> 140
<211> 190
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:1502670.1.orf2:2002JAN18

<400> 140
Ala Leu Ser Arg Gly Ala Glu Leu Arg Val Pro Gly Gly Ala Lys
1 5 10 15
His Gly Met Cys Leu Leu Leu Gly Ala Thr Gly Val Gly Lys Thr
20 25 30
Leu Leu Val Lys Arg Leu Gln Glu Val Ser Ser Arg Asp Gly Lys
35 40 45
Gly Asp Leu Gly Glu Pro Pro Pro Thr Arg Pro Thr Val Gly Thr
50 55 60
Asn Leu Thr Asp Ile Val Ala Gln Arg Lys Ile Thr Ile Arg Glu
65 70 75
Leu Gly Gly Cys Met Gly Pro Ile Trp Ser Ser Tyr Tyr Gly Asn
80 85 90
Cys Arg Ser Leu Leu Phe Val Met Asp Ala Ser Asp Pro Thr Gln
95 100 105
Leu Ser Ala Ser Cys Val Gln Leu Leu Gly Leu Leu Ser Ala Glu
110 115 120
Gln Leu Ala Glu Ala Ser Val Leu Ile Leu Phe Asn Lys Ile Asp
125 130 135
Leu Pro Cys Tyr Met Ser Thr Glu Glu Met Lys Ser Leu Ile Arg
140 145 150
Leu Pro Asp Ile Ile Ala Cys Ala Lys Gln Asn Ile Thr Thr Ala
155 160 165
Glu Ile Ser Ala Arg Glu Gly Thr Gly Leu Ala Gly Val Leu Ala
170 175 180
Trp Leu Gln Ala Thr His Arg Ala Asn Asp
185 190

<210> 141
<211> 153
<212> PRT

<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:206593.3.orf2:2002JAN18

<400> 141

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Leu Ser Thr Tyr Glu Leu Thr Leu Glu Arg Lys Pro Tyr Glu Cys
1               5                   10                  15
Lys Val Cys Gly Lys Ala Phe Thr Thr Ser Ser His Leu Ile Val
                20                  25                  30
His Ile Arg Ser His Thr Gly Glu Lys Pro Tyr Ile Cys Lys Glu
                35                  40                  45
Cys Gly Lys Ala Phe Ala Ser Ser Ser His Leu Ile Glu His Arg
                50                  55                  60
Arg Thr His Thr Gly Glu Lys Pro Tyr Ile Cys Asn Glu Cys Gly
                65                  70                  75
Lys Ala Phe Arg Ala Ser Ser His Leu His Lys His Gly Arg Ile
                80                  85                  90
His Thr Gly Gln Lys Pro Tyr Lys Cys Lys Glu Cys Gly Lys Ala
                95                  100                 105
Tyr Asn Arg Phe Tyr Leu Leu Lys Glu His Leu Lys Thr Tyr Thr
                110                 115                 120
Glu Glu Gln Val Phe Val Cys Lys Asp Cys Gly Lys Ser Phe Lys
                125                 130                 135
Asn Ser Ser Cys Leu Asn His His Thr Gln Ile His Thr Asp Glu
                140                 145                 150
Lys Pro Phe
```

<210> 142
<211> 608
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:228273.22.orf1:2002JAN18

<220>
<221> unsure
<222> (1) ... (608)
<223> unknown or other

<400> 142

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Gly Pro Gly Ser Asp Pro Arg Ala Ser Ser Gln Thr Met Arg Arg
1               5                   10                  15
Arg Ser Trp Asp Gln Ala Cys Leu Leu Gln Glu Lys Gln Glu Glu
                20                  25                  30
Gly Lys Asp Pro Glu Gly Gln Pro Leu Leu Ala Pro Gln Arg Val
                35                  40                  45
Arg Ser Gly Ala Ala Ala Xaa Leu Gln Gln Val Arg Thr Lys Glu
                50                  55                  60
Cys Trp Ser Trp Glu Ser Tyr Leu Glu Glu Gln Lys Ala Ile Thr
                65                  70                  75
Ala Pro Val Ser Leu Phe Gln Asp Ser Gln Ala Val Thr His Asn
                80                  85                  90
Lys Asn Gly Phe Lys Leu Gly Met Lys Leu Glu Gly Ile Asp Pro
                95                  100                 105
Gln His Pro Ser Met Tyr Phe Ile Leu Thr Val Ala Glu Val Cys
                110                 115                 120
Gly Tyr Arg Leu Arg Leu His Phe Asp Gly Tyr Ser Glu Cys His
                125                 130                 135
```

Asp Phe Trp Val Asn Ala Asn Ser Pro Asp Ile His Pro Ala Gly
140 145 150
Trp Phe Glu Lys Thr Gly His Lys Leu Gln Pro Pro Lys Gly Tyr
155 160 165
Lys Glu Glu Glu Phe Ser Trp Ser Gln Tyr Leu Arg Ser Thr Arg
170 175 180
Ala Gln Ala Ala Pro Lys His Leu Phe Val Ser Gln Ser His Ser
185 190 195
Pro Pro Pro Leu Gly Phe Gln Val Gly Met Lys Leu Glu Ala Val
200 205 210
Asp Arg Met Asn Pro Ser Leu Val Cys Val Ala Ser Val Thr Asp
215 220 225
Val Val Asp Ser Arg Phe Leu Val His Phe Asp Asn Trp Asp Asp
230 235 240
Thr Tyr Asp Tyr Trp Cys Asp Pro Ser Ser Pro Tyr Ile His Pro
245 250 255
Val Gly Trp Cys Gln Lys Gln Gly Lys Pro Leu Thr Pro Pro Gln
260 265 270
Asp Tyr Pro Asp Pro Asp Asn Phe Cys Trp Glu Lys Tyr Leu Glu
275 280 285
Glu Thr Gly Ala Ser Ala Val Pro Thr Trp Ala Phe Lys Val Arg
290 295 300
Pro Pro His Ser Phe Leu Val Asn Met Lys Leu Glu Ala Val Asp
305 310 315
Arg Arg Asn Pro Ala Leu Ile Arg Val Ala Ser Val Glu Asp Val
320 325 330
Glu Asp His Arg Ile Lys Ile His Phe Asp Gly Trp Ser His Gly
335 340 345
Tyr Asp Phe Trp Ile Asp Ala Asp His Pro Asp Ile His Pro Ala
350 355 360
Gly Trp Cys Ser Lys Thr Gly His Pro Leu Gln Pro Pro Leu Gly
365 370 375
Pro Arg Glu Pro Ser Ser Ala Ser Pro Gly Gly Cys Pro Pro Leu
380 385 390
Ser Tyr Arg Ser Leu Pro His Thr Arg Thr Ser Lys Tyr Ser Phe
395 400 405
His His Arg Lys Cys Pro Thr Pro Gly Cys Asp Gly Ser Gly His
410 415 420
Val Thr Gly Lys Phe Thr Ala His His Cys Leu Ser Gly Cys Pro
425 430 435
Leu Ala Glu Arg Asn Gln Ser Arg Leu Lys Ala Glu Leu Ser Asp
440 445 450
Ser Glu Ala Ser Ala Arg Lys Lys Asn Leu Ser Gly Phe Ser Pro
455 460 465
Arg Lys Lys Pro Arg His His Gly Arg Ile Gly Arg Pro Pro Lys
470 475 480
Tyr Arg Lys Ile Pro Gln Glu Asp Phe Gln Thr Leu Thr Pro Asp
485 490 495
Val Val His Gln Ser Leu Phe Met Ser Ala Leu Ser Ala His Pro
500 505 510
Asp Arg Ser Leu Ser Val Cys Trp Glu Gln His Cys Lys Leu Leu
515 520 525
Pro Gly Val Ala Gly Ile Ser Ala Ser Thr Val Ala Lys Trp Thr
530 535 540
Ile Asp Glu Val Phe Gly Phe Val Gln Thr Leu Thr Gly Cys Glu
545 550 555
Asp Gln Ala Arg Leu Phe Lys Asp Glu Met Ile Asp Gly Glu Ala
560 565 570
Phe Leu Leu Leu Thr Gln Ala Asp Ile Val Lys Ile Met Ser Val
575 580 585
Lys Leu Gly Pro Ala Leu Lys Ile Tyr Asn Ala Ile Leu Met Phe
590 595 600
Lys Asn Ala Asp Asp Thr Leu Lys

605

<210> 143
<211> 265
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:228319.2.orf1:2002JAN18

<400> 143
Glu Gln Ala Glu Glu Glu Lys Lys Pro Lys Asp Ser Thr Thr Pro
1 5 10 15
Leu Ser His Val Pro Ser Ala Ala Ala Gln Gly Ala Trp Ser Trp
20 25 30
Glu Trp Tyr Leu Lys Glu Gln Lys Ala Val Ala Ala Pro Val Glu
35 40 45
Leu Phe Ser Lys Asp Gln Ser Phe Pro Glu His Glu Asn Gly Phe
50 55 60
Gln Ile Gly Met Arg Leu Glu Gly Ile Asp Pro Arg His Pro Ser
65 70 75
Val Phe Cys Val Leu Ser Val Ala Glu Val Cys Gly Tyr Arg Leu
80 85 90
Arg Leu His Phe Asp Gly Tyr Leu Ser Cys Tyr Asp Phe Trp Thr
95 100 105
Asn Ala Gly Ser Pro Asp Ile His Pro Val Gly Trp Cys Glu Lys
110 115 120
Thr Lys His Glu Leu His Ile Pro Lys Gly Tyr Arg Lys Asp Lys
125 130 135
Phe Val Trp Met Asp Tyr Leu Lys Ala Cys Lys Leu Gln Asn Ala
140 145 150
Pro Lys Lys Leu Phe Arg Asn Arg Ser Pro Asn Gly Pro Met Ser
155 160 165
Lys Glu Phe Gln Val Gly Met Lys Leu Glu Ala Val Asp Arg Lys
170 175 180
Asn Pro Ser Leu Val Cys Val Ala Thr Ile Ala Asp Ile Val Glu
185 190 195
Asp Arg Leu Leu Val His Phe Asp Asn Trp Gly Asp Ser Tyr Asp
200 205 210
Tyr Trp Cys Asp Val Asn Ser Pro Tyr Val Gln Pro Val Gly Trp
215 220 225
Cys Gln Glu Asn Gly Arg Thr Leu Ile Ala Pro Gln Gly Tyr Pro
230 235 240
Ile Gln Lys Ile Phe Pro Gly Gln Asn Thr Trp Lys Leu Leu Lys
245 250 255
Pro Met Gln Phe Leu Pro Lys Phe Leu Lys
260 265

<210> 144
<211> 687
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:229165.16.orf2:2002JAN18

<400> 144
Tyr Gln Arg Gln Leu Lys Glu Met Asn Phe Glu Thr Ser Arg Cys
1 5 10 15
Ala Thr Leu Gln Tyr Cys Pro Asp Pro Tyr Ile Gln Arg Phe Val
20 25 30

Glu Thr Pro Ala His Phe Ser Trp Lys Glu Ser Tyr Tyr Arg Ser
35 40 45
Thr Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu
50 55 60
Val Phe Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser
65 70 75
Val Gln Pro Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp
80 85 90
Gly Ala Thr Asn Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met
95 100 105
Gln Asp Ser Asp Leu Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn
110 115 120
Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn Gly Ser
125 130 135
Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser Val
140 145 150
Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
155 160 165
Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly
170 175 180
Pro His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys
185 190 195
Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys
200 205 210
Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro
215 220 225
Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys
230 235 240
Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His Glu
245 250 255
Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
260 265 270
Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp
275 280 285
Pro Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro
290 295 300
Gln Val Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys
305 310 315
Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile
320 325 330
Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg
335 340 345
Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys
350 355 360
Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp Ser Thr
365 370 375
Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr His
380 385 390
Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp
395 400 405
Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met
410 415 420
Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro
425 430 435
Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln Gln Gln His
440 445 450
Gln His Leu Leu Gln Lys Gln Thr Ser Ile Gln Ser Pro Ser Ser
455 460 465
Tyr Gly Asn Ser Ser Pro Pro Leu Asn Lys Met Asn Ser Met Asn
470 475 480
Lys Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn
485 490 495
Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met Gly Ala Asn Ile

500 505 510
Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp Met Asn Gly
515 520 525
Leu Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met Pro Ser
530 535 540
Thr Ser His Cys Thr Pro Pro Pro Pro Tyr Pro Thr Asp Cys Ser
545 550 555
Ile Val Ser Phe Leu Ala Arg Leu Gly Cys Ser Ser Cys Leu Asp
560 565 570
Tyr Phe Thr Thr Gln Gly Leu Thr Thr Ile Tyr Gln Ile Glu His
575 580 585
Tyr Ser Met Asp Asp Leu Ala Ser Leu Lys Ile Pro Glu Gln Phe
590 595 600
Arg His Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln Leu His
605 610 615
Glu Phe Ser Ser Pro Ser His Leu Leu Arg Thr Pro Ser Ser Ala
620 625 630
Ser Thr Val Ser Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val
635 640 645
Ile Asp Ala Val Arg Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro
650 655 660
Pro Arg Asp Glu Trp Asn Asp Phe Asn Phe Asp Met Asp Ala Arg
665 670 675
Arg Asn Lys Gln Gln Arg Ile Lys Glu Glu Gly Glu
680 685

<210> 145
<211> 478
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:230895.9.orf1:2002JAN18

<400> 145
Asn Arg Ser Leu Pro Asp Val Arg Leu Glu Gly Cys Lys Thr Lys
1 5 10 15
Val Tyr Pro Asp Glu Leu Pro Asn Thr Ser Val Val Ile Val Phe
20 25 30
His Asn Glu Ala Trp Ser Thr Leu Leu Arg Thr Val Tyr Ser Val
35 40 45
Ile Asn Arg Ser Pro His Tyr Leu Leu Ser Glu Val Ile Leu Val
50 55 60
Asp Asp Ala Ser Glu Arg Asp Phe Leu Lys Leu Thr Leu Glu Asn
65 70 75
Tyr Val Lys Asn Leu Glu Val Pro Val Lys Ile Ile Arg Met Glu
80 85 90
Glu Arg Ser Gly Leu Ile Arg Ala Arg Leu Arg Gly Ala Ala Ala
95 100 105
Ser Lys Gly Gln Val Ile Thr Phe Leu Asp Ala His Cys Glu Cys
110 115 120
Thr Leu Gly Trp Leu Glu Pro Leu Leu Ala Arg Ile Lys Glu Asp
125 130 135
Arg Lys Thr Val Val Cys Pro Ile Ile Asp Val Ile Ser Asp Asp
140 145 150
Thr Phe Glu Tyr Met Ala Gly Ser Asp Met Thr Tyr Gly Gly Phe
155 160 165
Asn Trp Lys Leu Asn Phe Arg Trp Tyr Pro Val Pro Gln Arg Glu
170 175 180
Met Asp Arg Arg Lys Gly Asp Arg Thr Leu Pro Val Arg Thr Pro
185 190 195
Thr Met Ala Gly Gly Leu Phe Ser Ile Asp Arg Asn Tyr Phe Glu

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                    200                     205                     210
Glu Ile Gly Thr Tyr Asp Ala Gly Met Asp Ile Trp Gly Gly Glu
                    215                     220                     225
Asn Leu Glu Met Ser Phe Arg Ile Trp Gln Cys Gly Gly Ser Leu
                    230                     235                     240
Glu Ile Val Thr Cys Ser His Val Gly His Val Phe Arg Lys Ala
                    245                     250                     255
Thr Pro Tyr Thr Phe Pro Gly Gly Thr Gly His Val Ile Asn Lys
                    260                     265                     270
Asn Asn Arg Arg Leu Ala Glu Val Trp Met Asp Glu Phe Lys Asp
                    275                     280                     285
Phe Phe Tyr Ile Ile Ser Pro Gly Val Val Lys Val Asp Tyr Gly
                    290                     295                     300
Asp Val Ser Val Arg Lys Thr Leu Arg Glu Asn Leu Lys Cys Lys
                    305                     310                     315
Pro Phe Ser Trp Tyr Leu Glu Asn Ile Tyr Pro Asp Ser Gln Ile
                    320                     325                     330
Pro Arg Arg Tyr Tyr Ser Leu Gly Glu Ile Arg Asn Val Glu Thr
                    335                     340                     345
Asn Gln Cys Leu Asp Asn Met Gly Arg Lys Glu Asn Glu Lys Val
                    350                     355                     360
Gly Ile Phe Asn Cys His Gly Met Gly Gly Asn Gln Val Phe Ser
                    365                     370                     375
Tyr Thr Ala Asp Lys Glu Ile Arg Thr Asp Asp Leu Cys Leu Asp
                    380                     385                     390
Val Ser Arg Leu Asn Gly Pro Val Ile Met Leu Lys Cys His His
                    395                     400                     405
Met Arg Gly Asn Gln Leu Trp Glu Tyr Asp Ala Glu Thr His Thr
                    410                     415                     420
Leu Leu His Ile Ile Thr Gln Ser Cys Leu Ser Val Asn Lys Val
                    425                     430                     435
Ala Asp Gly Ser Gln His Pro Thr Val Glu Thr Cys Asn Asp Ser
                    440                     445                     450
Thr Leu Gln Lys Trp Leu Leu Arg Asn Tyr Thr Arg Met Glu Ile
                    455                     460                     465
Phe Arg Asn Ile Phe Gly Asn Ser Thr Asp Tyr Ile Leu
                    470                     475
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<210> 146
<211> 946
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:233552.5.orf1:2002JAN18

<400> 146

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Val Met Phe Ala Asp Arg Lys Ser Lys Leu Ser Arg Glu Phe Arg
 1               5                  10                  15
Ala Leu Gly Thr Cys Tyr Leu Asp Gln Phe Glu Ala Ser Leu Ile
                20                  25                  30
Tyr Trp Thr Asn Trp Gln Gln Lys Met Lys Ser Ser Val Ala Gln
                35                  40                  45
Ile Lys Pro Ser Ser Gly His Asp Arg Arg Glu Asn Leu Asn Pro
                50                  55                  60
Tyr Gln Arg Asn Ser Ser Pro Glu Asp Arg Tyr Glu Glu Gln Glu
                65                  70                  75
Arg Ser Pro Arg Asp Arg Asp Tyr Phe Asp Tyr Ser Arg Ser Asp
                80                  85                  90
Tyr Glu His Ser Arg Arg Gly Arg Ser Tyr Asp Ser Ser Met Glu
                95                 100                 105
Ser Arg Asn Arg Asp Arg Glu Lys Arg Arg Glu Arg Glu Arg Asp
```

110 115 120
Thr Asp Arg Lys Arg Ser Arg Lys Ser Pro Ser Pro Gly Arg Arg
125 130 135
Asn Pro Glu Thr Ser Val Thr Gln Ser Ser Ser Ala Gln Asp Glu
140 145 150
Pro Ala Thr Lys Lys Lys Lys Asp Glu Leu Asp Pro Leu Leu Thr
155 160 165
Arg Thr Gly Gly Ala Tyr Ile Pro Pro Ala Lys Leu Arg Met Met
170 175 180
Gln Glu Gln Ile Thr Asp Lys Asn Ser Leu Ala Tyr Gln Arg Met
185 190 195
Ser Trp Glu Ala Leu Lys Lys Ser Ile Asn Gly Leu Ile Asn Lys
200 205 210
Val Asn Ile Ser Asn Ile Ser Ile Ile Ile Gln Glu Leu Leu Gln
215 220 225
Glu Asn Ile Val Arg Gly Arg Gly Leu Leu Ser Arg Ser Val Leu
230 235 240
Gln Ala Gln Ser Ala Ser Pro Ile Phe Thr His Val Tyr Ala Ala
245 250 255
Leu Val Ala Ile Ile Asn Ser Lys Phe Pro Gln Ile Gly Glu Leu
260 265 270
Ile Leu Lys Arg Leu Ile Leu Asn Phe Arg Lys Gly Tyr Arg Arg
275 280 285
Asn Asp Lys Gln Leu Cys Leu Thr Ala Ser Lys Phe Val Ala His
290 295 300
Leu Ile Asn Gln Asn Val Ala His Glu Val Leu Cys Leu Glu Met
305 310 315
Leu Thr Leu Leu Leu Glu Arg Pro Thr Asp Asp Ser Val Glu Val
320 325 330
Ala Ile Gly Phe Leu Lys Glu Cys Gly Leu Lys Leu Thr Gln Val
335 340 345
Ser Pro Arg Gly Ile Asn Ala Ile Phe Glu Arg Leu Arg Asn Ile
350 355 360
Leu His Glu Ser Glu Ile Asp Lys Arg Val Gln Tyr Met Ile Glu
365 370 375
Val Met Phe Ala Val Arg Lys Asp Gly Phe Lys Asp His Pro Ile
380 385 390
Ile Leu Glu Gly Leu Asp Leu Val Glu Glu Asp Asp Gln Phe Thr
395 400 405
His Met Leu Pro Leu Glu Asp Asp Tyr Asn Pro Glu Asp Val Leu
410 415 420
Asn Val Phe Lys Met Asp Pro Asn Phe Met Glu Asn Glu Glu Lys
425 430 435
Tyr Lys Ala Ile Lys Lys Glu Ile Leu Asp Glu Gly Asp Thr Asp
440 445 450
Ser Asn Thr Asp Gln Asp Ala Gly Ser Ser Glu Glu Asp Glu Glu
455 460 465
Glu Glu Glu Glu Glu Gly Glu Glu Asp Glu Glu Gly Gln Lys Val
470 475 480
Thr Ile His Asp Lys Thr Glu Ile Asn Leu Val Ser Phe Arg Arg
485 490 495
Thr Ile Tyr Leu Ala Ile Gln Ser Ser Leu Asp Phe Glu Glu Cys
500 505 510
Ala His Lys Leu Leu Lys Met Glu Phe Pro Glu Ser Gln Thr Lys
515 520 525
Glu Leu Cys Asn Met Ile Leu Asp Cys Cys Ala Gln Gln Arg Thr
530 535 540
Tyr Glu Lys Phe Phe Gly Leu Leu Ala Gly Arg Phe Cys Met Leu
545 550 555
Lys Lys Glu Tyr Met Glu Ser Phe Glu Gly Ile Phe Lys Glu Gln
560 565 570
Tyr Asp Thr Ile His Arg Leu Glu Thr Asn Lys Leu Arg Asn Val
575 580 585

Ala Lys Met Phe Ala His Leu Leu Tyr Thr Asp Ser Leu Pro Trp
590 595 600
Ser Val Leu Glu Cys Ile Lys Leu Ser Glu Glu Thr Thr Thr Ser
605 610 615
Ser Ser Arg Ile Phe Val Lys Ile Phe Phe Gln Glu Leu Cys Glu
620 625 630
Tyr Met Gly Leu Pro Lys Leu Asn Ala Arg Leu Lys Asp Glu Thr
635 640 645
Leu Gln Pro Phe Phe Glu Gly Leu Leu Pro Arg Asp Asn Pro Arg
650 655 660
Asn Thr Arg Phe Ala Ile Asn Phe Phe Thr Ser Ile Gly Leu Gly
665 670 675
Gly Leu Thr Asp Glu Leu Arg Glu His Leu Lys Asn Thr Pro Lys
680 685 690
Val Ile Val Ala Gln Lys Pro Asp Val Glu Gln Asn Lys Ser Ser
695 700 705
Pro Ser Ser Ser Ser Ser Ala Ser Ser Ser Ser Glu Ser Asp Ser
710 715 720
Ser Asp Ser Asp Ser Asp Ser Ser Asp Ser Ser Ser Glu Ser Ser
725 730 735
Ser Glu Glu Ser Asp Ser Ser Ser Ile Ser Ser His Ser Ser Ala
740 745 750
Ser Ala Asn Asp Val Arg Lys Lys Gly His Gly Lys Thr Arg Ser
755 760 765
Lys Glu Val Asp Lys Leu Ile Arg Asn Gln Gln Thr Asn Asp Arg
770 775 780
Lys Gln Lys Glu Arg Arg Gln Glu His Gly His Gln Glu Thr Arg
785 790 795
Thr Glu Arg Glu Arg Arg Ser Glu Lys His Arg Asp Gln Asn Ser
800 805 810
Arg Gly Ser Asn Trp Arg Asp Pro Ile Thr Lys Tyr Thr Ser Asp
815 820 825
Lys Asp Val Pro Ser Glu Arg Asn Asn Tyr Ser Arg Val Ala Asn
830 835 840
Asp Arg Asp Gln Glu Met His Ile Asp Leu Glu Asn Lys His Gly
845 850 855
Asp Pro Lys Lys Lys Arg Gly Glu Arg Arg Asn Ser Phe Ser Glu
860 865 870
Asn Glu Lys His Thr His Arg Ile Lys Asp Ser Glu Asn Phe Arg
875 880 885
Arg Lys Asp Arg Ser Lys Ser Lys Glu Met Asn Arg Lys His Ser
890 895 900
Gly Ser Arg Ser Asp Glu Asp Arg Tyr Gln Asn Gly Ala Glu Arg
905 910 915
Arg Trp Glu Lys Ser Ser Arg Tyr Ser Glu Gln Ser Arg Glu Ser
920 925 930
Lys Lys Asn Gln Asp Arg Arg Arg Glu Lys Ser Pro Ala Lys Gln
935 940 945
Lys

<210> 147
<211> 318
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:234430.7.orf3:2002JAN18

<400> 147
Gly Val Glu Ser Ala Pro Cys Pro Arg Arg Glu Arg Gly Ala Gly
1 5 10 15

Gly Arg Arg Pro Ala Gly Cys Met Ala Arg Cys Glu Arg Leu Arg
20 25 30
Gly Ala Ala Leu Arg Asp Val Leu Gly Arg Ala Gln Gly Val Leu
35 40 45
Phe Asp Cys Asp Gly Val Leu Trp Asn Gly Glu Arg Ala Val Pro
50 55 60
Gly Ala Pro Glu Leu Leu Glu Arg Leu Ala Arg Ala Gly Lys Ala
65 70 75
Ala Leu Phe Val Ser Asn Asn Ser Arg Arg Ala Arg Pro Glu Leu
80 85 90
Ala Leu Arg Phe Ala Arg Leu Gly Phe Gly Gly Leu Arg Ala Glu
95 100 105
Gln Leu Phe Ser Ser Ala Leu Cys Ala Ala Arg Leu Leu Arg Gln
110 115 120
Arg Leu Pro Gly Pro Pro Asp Ala Pro Gly Ala Val Phe Val Leu
125 130 135
Gly Gly Glu Gly Leu Arg Ala Glu Leu Arg Ala Ala Gly Leu Arg
140 145 150
Leu Ala Gly Asp Pro Ser Ala Gly Asp Gly Ala Ala Pro Arg Val
155 160 165
Arg Ala Val Leu Val Gly Tyr Asp Glu His Phe Ser Phe Ala Lys
170 175 180
Leu Arg Glu Ala Cys Ala His Leu Arg Asp Pro Glu Cys Leu Leu
185 190 195
Val Ala Thr Asp Arg Asp Pro Trp His Pro Leu Ser Asp Gly Ser
200 205 210
Arg Thr Pro Gly Thr Gly Ser Leu Ala Ala Ala Val Glu Thr Ala
215 220 225
Ser Gly Arg Gln Ala Leu Val Val Gly Lys Pro Ser Pro Tyr Met
230 235 240
Phe Glu Cys Ile Thr Glu Asn Phe Ser Ile Asp Pro Ala Arg Thr
245 250 255
Leu Met Val Gly Asp Arg Leu Glu Thr Asp Ile Leu Phe Gly His
260 265 270
Arg Cys Gly Met Thr Thr Val Leu Thr Leu Thr Gly Val Ser Arg
275 280 285
Leu Glu Glu Ala Gln Ala Tyr Leu Ala Ala Gly Gln His Asp Leu
290 295 300
Val Pro His Tyr Tyr Val Glu Ser Ile Ala Asp Leu Thr Glu Gly
305 310 315
Leu Glu Asp

<210> 148
<211> 1632
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:236659.1.orf3:2002JAN18

<400> 148
Glu Val Arg Ala Ala Gly Ala Glu Ala Thr Ala Ala Ala Ala Ala
1 5 10 15
Gly Gly Ala Ile Ala Ala Ala Val Ala Ala Thr Gly Arg Gly Ala
20 25 30
Ala Val Gly Asp Arg Gly Arg Gly Cys Arg Arg Arg Ser Gly Trp
35 40 45
Lys Lys Leu Asp Ser Met Gly Ser Lys Arg Arg Arg Ala Thr Ser
50 55 60
Pro Ser Ser Ser Val Ser Gly Asp Phe Asp Asp Gly His His Ser
65 70 75

Val Ser Thr Pro Gly Pro Ser Arg Lys Arg Arg Arg Leu Ser Asn
80 85 90
Leu Pro Thr Val Asp Pro Ile Ala Val Cys His Glu Leu Tyr Asn
95 100 105
Thr Ile Arg Asp Tyr Lys Asp Glu Gln Gly Arg Leu Leu Cys Glu
110 115 120
Leu Phe Ile Arg Ala Pro Lys Arg Arg Asn Gln Pro Asp Tyr Tyr
125 130 135
Glu Val Val Ser Gln Pro Ile Asp Leu Met Lys Ile Gln Gln Lys
140 145 150
Leu Lys Met Glu Glu Tyr Asp Asp Val Asn Leu Leu Thr Ala Asp
155 160 165
Phe Gln Leu Leu Phe Asn Asn Ala Lys Ser Tyr Tyr Lys Pro Asp
170 175 180
Ser Pro Glu Tyr Lys Ala Ala Cys Lys Leu Trp Asp Leu Tyr Leu
185 190 195
Arg Thr Arg Asn Glu Phe Val Gln Lys Gly Glu Ala Asp Asp Glu
200 205 210
Asp Asp Asp Glu Asp Gly Gln Asp Asn Gln Gly Thr Val Thr Glu
215 220 225
Gly Ser Ser Pro Ala Tyr Leu Lys Glu Ile Leu Glu Gln Leu Leu
230 235 240
Glu Ala Ile Val Val Ala Thr Asn Pro Ser Gly Arg Leu Ile Ser
245 250 255
Glu Leu Phe Gln Lys Leu Pro Ser Lys Val Gln Tyr Pro Asp Tyr
260 265 270
Tyr Ala Ile Ile Lys Glu Pro Ile Asp Leu Lys Thr Ile Ala Gln
275 280 285
Arg Ile Gln Asn Gly Ser Tyr Lys Ser Ile His Ala Met Ala Lys
290 295 300
Asp Ile Asp Leu Leu Ala Lys Asn Ala Lys Thr Tyr Asn Glu Pro
305 310 315
Gly Ser Gln Val Phe Lys Asp Ala Asn Ser Ile Lys Lys Ile Phe
320 325 330
Tyr Met Lys Lys Ala Glu Ile Glu His His Glu Met Ala Lys Ser
335 340 345
Ser Leu Arg Met Arg Thr Pro Ser Asn Leu Ala Ala Ala Arg Leu
350 355 360
Thr Gly Pro Ser His Ser Lys Gly Ser Leu Gly Glu Glu Arg Asn
365 370 375
Pro Thr Ser Lys Tyr Tyr Arg Asn Lys Arg Ala Val Gln Gly Gly
380 385 390
Arg Leu Ser Ala Ile Thr Met Ala Leu Gln Tyr Gly Ser Glu Ser
395 400 405
Glu Glu Asp Ala Ala Leu Ala Ala Ala Arg Tyr Glu Glu Gly Glu
410 415 420
Ser Glu Ala Glu Ser Ile Thr Ser Phe Met Asp Val Ser Asn Pro
425 430 435
Phe Tyr Gln Leu Tyr Asp Thr Val Arg Ser Cys Arg Asn Asn Gln
440 445 450
Gly Gln Leu Ile Ala Glu Pro Phe Tyr His Leu Pro Ser Lys Lys
455 460 465
Lys Tyr Pro Asp Tyr Tyr Gln Gln Ile Lys Met Pro Ile Ser Leu
470 475 480
Gln Gln Ile Arg Thr Lys Leu Lys Asn Gln Glu Tyr Glu Thr Leu
485 490 495
Asp His Leu Glu Cys Asp Leu Asn Leu Met Phe Glu Asn Ala Lys
500 505 510
Arg Tyr Asn Val Pro Asn Ser Ala Ile Tyr Lys Arg Val Leu Lys
515 520 525
Leu Gln Gln Val Met Gln Ala Lys Lys Lys Glu Leu Ala Arg Arg
530 535 540
Asp Asp Ile Glu Asp Gly Asp Ser Met Ile Ser Ser Ala Thr Ser

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                545                      550                      555
Asp Thr Gly Ser Ala Lys Arg Lys Ser Lys Lys Asn Ile Arg Lys
                560                      565                      570
Gln Arg Met Lys Ile Leu Phe Asn Val Val Leu Glu Ala Arg Glu
                575                      580                      585
Pro Gly Ser Gly Arg Arg Leu Cys Asp Leu Phe Met Val Lys Pro
                590                      595                      600
Ser Lys Lys Asp Tyr Pro Asp Tyr Tyr Lys Ile Ile Leu Glu Pro
                605                      610                      615
Met Asp Leu Lys Ile Ile Glu His Asn Ile Arg Asn Asp Lys Tyr
                620                      625                      630
Ala Gly Glu Glu Gly Met Ile Glu Asp Met Lys Leu Met Phe Arg
                635                      640                      645
Asn Ala Arg His Tyr Asn Glu Glu Gly Ser Gln Val Tyr Asn Asp
                650                      655                      660
Ala His Ile Leu Glu Lys Leu Leu Lys Glu Lys Arg Lys Glu Leu
                665                      670                      675
Gly Pro Leu Pro Asp Asp Asp Asp Met Ala Ser Pro Lys Leu Lys
                680                      685                      690
Leu Ser Arg Lys Ser Gly Ile Ser Pro Lys Lys Ser Lys Tyr Met
                695                      700                      705
Thr Pro Met Gln Gln Lys Leu Asn Glu Val Tyr Glu Ala Val Lys
                710                      715                      720
Asn Tyr Thr Asp Lys Arg Gly Arg Arg Leu Ser Ala Ile Phe Leu
                725                      730                      735
Arg Leu Pro Ser Arg Ser Glu Leu Pro Asp Tyr Tyr Leu Thr Ile
                740                      745                      750
Lys Lys Pro Met Asp Met Glu Lys Ile Arg Ser His Met Met Ala
                755                      760                      765
Asn Lys Tyr Gln Asp Ile Asp Ser Met Val Glu Asp Phe Val Met
                770                      775                      780
Met Phe Asn Asn Ala Cys Thr Tyr Asn Glu Pro Glu Ser Leu Ile
                785                      790                      795
Tyr Lys Asp Ala Leu Val Leu His Lys Val Leu Leu Glu Thr Arg
                800                      805                      810
Arg Asp Leu Glu Gly Asp Glu Asp Ser His Val Pro Asn Val Thr
                815                      820                      825
Leu Leu Ile Gln Glu Leu Ile His Asn Leu Phe Val Ser Val Met
                830                      835                      840
Ser His Gln Asp Asp Glu Gly Arg Cys Tyr Ser Asp Ser Leu Ala
                845                      850                      855
Glu Ile Pro Ala Val Asp Pro Asn Phe Pro Asn Lys Pro Pro Leu
                860                      865                      870
Thr Phe Asp Ile Ile Arg Lys Asn Val Glu Asn Asn Arg Tyr Arg
                875                      880                      885
Arg Leu Asp Leu Phe Gln Glu His Met Phe Glu Val Leu Glu Arg
                890                      895                      900
Ala Arg Arg Met Asn Arg Thr Asp Ser Glu Ile Tyr Glu Asp Ala
                905                      910                      915
Val Glu Leu Gln Gln Phe Phe Ile Lys Ile Arg Asp Glu Leu Cys
                920                      925                      930
Lys Asn Gly Glu Ile Leu Leu Ser Pro Ala Leu Ser Tyr Thr Thr
                935                      940                      945
Lys His Leu His Asn Asp Val Glu Lys Glu Arg Lys Glu Lys Leu
                950                      955                      960
Pro Lys Glu Ile Glu Glu Asp Lys Leu Lys Arg Glu Glu Glu Lys
                965                      970                      975
Arg Glu Ala Glu Lys Ser Glu Asp Ser Ser Gly Ala Ala Gly Leu
                980                      985                      990
Ser Gly Leu His Arg Thr Tyr Ser Gln Asp Cys Ser Phe Lys Asn
                995                     1000                     1005
Ser Met Tyr His Val Gly Asp Tyr Val Tyr Val Glu Pro Ala Glu
               1010                     1015                     1020
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Ala Asn Leu Gln Pro His Ile Val Cys Ile Glu Arg Leu Trp Glu
1025 1030 1035
Asp Ser Ala Gly Glu Lys Trp Leu Tyr Gly Cys Trp Phe Tyr Arg
1040 1045 1050
Pro Asn Glu Thr Phe His Leu Ala Thr Arg Lys Phe Leu Glu Lys
1055 1060 1065
Glu Val Phe Lys Ser Asp Tyr Tyr Asn Lys Val Pro Val Ser Lys
1070 1075 1080
Ile Leu Gly Lys Cys Val Val Met Phe Val Lys Glu Tyr Phe Lys
1085 1090 1095
Leu Cys Pro Glu Asn Phe Arg Asp Glu Asp Val Phe Val Cys Glu
1100 1105 1110
Ser Arg Tyr Ser Ala Lys Thr Lys Ser Phe Lys Lys Ile Lys Leu
1115 1120 1125
Trp Thr Met Pro Ile Ser Ser Val Arg Phe Val Pro Arg Asp Val
1130 1135 1140
Pro Leu Pro Val Val Arg Val Ala Ser Val Phe Ala Asn Ala Asp
1145 1150 1155
Lys Gly Asp Asp Glu Lys Asn Thr Asp Asn Ser Glu Asp Ser Arg
1160 1165 1170
Ala Glu Asp Asn Phe Asn Leu Glu Lys Glu Lys Glu Asp Val Pro
1175 1180 1185
Val Glu Met Ser Asn Gly Glu Pro Gly Cys His Tyr Phe Glu Gln
1190 1195 1200
Leu His Tyr Asn Asp Met Trp Leu Lys Val Gly Asp Cys Val Phe
1205 1210 1215
Ile Lys Ser His Gly Leu Val Arg Pro Arg Val Gly Arg Ile Glu
1220 1225 1230
Lys Val Trp Val Arg Asp Gly Ala Ala Tyr Phe Tyr Gly Pro Ile
1235 1240 1245
Phe Ile His Pro Glu Glu Thr Glu His Glu Pro Thr Lys Met Phe
1250 1255 1260
Tyr Lys Lys Glu Val Phe Leu Ser Asn Leu Glu Glu Thr Cys Pro
1265 1270 1275
Met Thr Cys Ile Leu Gly Lys Cys Ala Val Leu Ser Phe Lys Asp
1280 1285 1290
Phe Leu Ser Cys Arg Pro Thr Glu Ile Pro Glu Asn Asp Ile Leu
1295 1300 1305
Leu Cys Glu Ser Arg Tyr Asn Glu Ser Asp Lys Gln Met Lys Lys
1310 1315 1320
Phe Lys Gly Leu Lys Arg Phe Ser Leu Ser Ala Lys Val Val Asp
1325 1330 1335
Asp Glu Ile Tyr Tyr Phe Arg Lys Pro Ile Val Pro Gln Lys Glu
1340 1345 1350
Pro Ser Pro Leu Leu Glu Lys Lys Ile Gln Leu Leu Glu Ala Lys
1355 1360 1365
Phe Ala Glu Leu Glu Gly Gly Asp Asp Asp Ile Glu Glu Met Gly
1370 1375 1380
Glu Glu Asp Ser Glu Val Ile Glu Pro Pro Ser Leu Pro Gln Leu
1385 1390 1395
Gln Thr Pro Leu Ala Ser Glu Leu Asp Leu Met Pro Tyr Thr Pro
1400 1405 1410
Pro Gln Ser Thr Pro Lys Ser Ala Lys Gly Ser Ala Lys Lys Glu
1415 1420 1425
Gly Ser Lys Arg Lys Ile Asn Met Ser Gly Tyr Ile Leu Phe Ser
1430 1435 1440
Ser Glu Met Arg Ala Val Ile Lys Ala Gln His Pro Asp Tyr Ser
1445 1450 1455
Phe Gly Glu Leu Ser Arg Leu Val Gly Thr Glu Trp Arg Asn Leu
1460 1465 1470
Glu Thr Ala Lys Lys Ala Glu Tyr Glu Gly Val Met Asn Gln Gly
1475 1480 1485
Val Ala Pro Met Val Gly Thr Pro Ala Pro Gly Gly Ser Pro Tyr

1490 1495 1500
Gly Gln Gln Val Gly Val Leu Gly Pro Pro Gly Gln Gln Ala Pro
1505 1510 1515
Pro Pro Tyr Pro Gly Pro His Pro Ala Gly Pro Pro Val Ile Gln
1520 1525 1530
Gln Pro Thr Thr Pro Met Phe Val Ala Pro Pro Pro Lys Thr Gln
1535 1540 1545
Arg Leu Leu His Ser Glu Ala Tyr Leu Lys Tyr Ile Glu Gly Leu
1550 1555 1560
Ser Ala Glu Ser Asn Ser Ile Ser Lys Trp Asp Gln Thr Leu Ala
1565 1570 1575
Ala Arg Arg Arg Asp Val His Leu Ser Lys Glu Gln Glu Ser Arg
1580 1585 1590
Leu Pro Ser His Trp Leu Lys Ser Lys Gly Ala His Thr Thr Met
1595 1600 1605
Ala Asp Ala Leu Trp Arg Leu Arg Asp Leu Met Leu Arg Asp Thr
1610 1615 1620
Leu Asn Ile Arg Gln Ala Tyr Asn Leu Glu Asn Val
1625 1630

<210> 149
<211> 736
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:236767.26.orf2:2002JAN18

<400> 149
Ala Gly Phe Pro Lys Met Ala Ala Asp Val Ser Val Thr His Arg
1 5 10 15
Pro Pro Leu Ser Pro Lys Ser Gly Ala Glu Val Glu Ala Gly Asp
20 25 30
Ala Ala Glu Arg Arg Ala Pro Glu Glu Glu Leu Pro Pro Leu Asp
35 40 45
Pro Glu Glu Ile Arg Lys Arg Leu Glu His Thr Glu Arg Gln Phe
50 55 60
Arg Asn Arg Arg Lys Ile Leu Ile Arg Gly Leu Pro Gly Asp Val
65 70 75
Thr Asn Gln Glu Val His Asp Leu Leu Ser Asp Tyr Glu Leu Lys
80 85 90
Tyr Cys Phe Val Asp Lys Tyr Lys Gly Thr Ala Phe Val Thr Leu
95 100 105
Leu Asn Gly Glu Gln Ala Glu Ala Ala Ile Asn Ala Phe His Gln
110 115 120
Ser Arg Leu Arg Glu Arg Glu Leu Ser Val Gln Leu Gln Pro Thr
125 130 135
Asp Ala Leu Leu Cys Val Ala Asn Leu Pro Pro Ser Leu Thr Gln
140 145 150
Gln Gln Phe Glu Glu Leu Val Arg Pro Phe Gly Ser Leu Glu Arg
155 160 165
Cys Phe Leu Val Tyr Ser Glu Arg Thr Gly Gln Ser Lys Gly Tyr
170 175 180
Gly Phe Ala Glu Tyr Met Lys Lys Asp Ser Ala Ala Arg Ala Lys
185 190 195
Ser Asp Leu Leu Gly Lys Pro Leu Gly Pro Arg Thr Leu Tyr Val
200 205 210
His Trp Thr Asp Ala Gly Gln Leu Thr Pro Ala Leu Leu His Ser
215 220 225
Arg Cys Leu Cys Val Asp Arg Leu Pro Pro Gly Phe Asn Asp Val
230 235 240
Asp Ala Leu Cys Arg Ala Leu Ser Ala Val His Ser Pro Thr Phe

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                245                     250                     255
Cys Gln Leu Ala Cys Gly Gln Asp Gly Gln Leu Lys Gly Phe Ala
                260                     265                     270
Val Leu Glu Tyr Glu Thr Ala Glu Met Ala Glu Glu Ala Gln Gln
                275                     280                     285
Gln Ala Asp Gly Leu Ser Leu Gly Gly Ser His Leu Arg Val Ser
                290                     295                     300
Phe Cys Ala Pro Gly Pro Pro Gly Arg Ser Met Leu Ala Ala Leu
                305                     310                     315
Ile Ala Ala Gln Ala Thr Ala Leu Asn Arg Gly Lys Gly Leu Leu
                320                     325                     330
Pro Glu Pro Asn Ile Leu Gln Leu Leu Asn Asn Leu Gly Pro Ser
                335                     340                     345
Ala Ser Leu Gln Leu Leu Leu Asn Pro Leu Leu His Gly Ser Ala
                350                     355                     360
Gly Gly Lys Gln Gly Leu Leu Gly Ala Pro Pro Ala Met Pro Leu
                365                     370                     375
Leu Asn Gly Pro Ala Leu Ser Thr Ala Leu Leu Gln Leu Ala Leu
                380                     385                     390
Gln Thr Gln Gly Gln Lys Lys Pro Gly Ile Leu Gly Asp Ser Pro
                395                     400                     405
Leu Gly Ala Leu Gln Pro Gly Ala Gln Pro Ala Asn Pro Leu Leu
                410                     415                     420
Gly Glu Leu Pro Ala Gly Gly Gly Leu Pro Pro Glu Leu Pro Pro
                425                     430                     435
Arg Arg Gly Lys Pro Pro Pro Leu Leu Pro Ser Val Leu Gly Pro
                440                     445                     450
Ala Gly Gly Asp Arg Glu Ala Leu Gly Leu Gly Pro Pro Ala Ala
                455                     460                     465
Gln Leu Thr Pro Pro Pro Ala Pro Val Gly Leu Arg Gly Ser Gly
                470                     475                     480
Leu Arg Gly Leu Gln Lys Asp Ser Gly Pro Leu Pro Thr Pro Pro
                485                     490                     495
Gly Val Ser Leu Leu Gly Glu Pro Pro Lys Asp Tyr Arg Ile Pro
                500                     505                     510
Leu Asn Pro Tyr Leu Asn Leu His Ser Leu Leu Pro Ala Ser Asn
                515                     520                     525
Leu Ala Gly Lys Glu Ala Arg Gly Trp Gly Gly Ala Gly Arg Ser
                530                     535                     540
Arg Arg Pro Ala Glu Gly Pro Pro Thr Asn Pro Pro Ala Pro Gly
                545                     550                     555
Gly Gly Ser Ser Ser Ser Lys Ala Phe Gln Leu Lys Ser Arg Leu
                560                     565                     570
Leu Ser Pro Leu Ser Ser Ala Arg Leu Pro Pro Glu Pro Gly Leu
                575                     580                     585
Ser Asp Ser Tyr Ser Phe Asp Tyr Pro Ser Asp Met Gly Pro Arg
                590                     595                     600
Arg Leu Phe Ser His Pro Arg Glu Pro Ala Leu Gly Pro His Gly
                605                     610                     615
Pro Ser Arg His Lys Met Ser Pro Pro Pro Ser Gly Phe Gly Glu
                620                     625                     630
Arg Ser Ser Gly Gly Ser Gly Gly Gly Pro Leu Ser His Phe Tyr
                635                     640                     645
Ser Gly Ser Pro Thr Ser Tyr Phe Thr Ser Gly Leu Gln Ala Gly
                650                     655                     660
Leu Lys Gln Ser His Leu Ser Lys Ala Ile Gly Ser Ser Pro Leu
                665                     670                     675
Gly Ser Gly Glu Gly Leu Leu Gly Leu Ser Pro Gly Pro Asn Gly
                680                     685                     690
His Ser His Leu Leu Lys Thr Pro Leu Gly Gly Arg Asn Ala Ala
                695                     700                     705
Leu Pro Thr Cys Cys Pro Arg Pro Ser Pro Ala Gln Lys Ala Ala
                710                     715                     720
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Met Trp Ala Ser Thr Pro Arg Pro Arg Arg His Tyr Ala Asp Ser
725 730 735

Thr

<210> 150
<211> 323
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:237489.7.orf1:2002JAN18

<400> 150
Gly Cys Thr Asn Arg Glu Trp Pro Trp Leu Ile Gln Glu Asp Phe
1 5 10 15
Leu Lys Glu Val Val Phe Ser Pro Gly Leu Leu Leu Thr Ser Leu
20 25 30
Phe Ser Gln Cys Ile Trp Val Val Ser Phe Leu Ser Ser Phe Phe
35 40 45
Leu Ser Leu Pro Tyr Gly Val Ala Val Gly Val Ala Phe Ser Val
50 55 60
Leu Val Val Val Phe Gln Thr Gln Phe Arg Asn Gly Tyr Ala Leu
65 70 75
Ala Gln Val Met Asp Thr Asp Ile Tyr Val Asn Pro Lys Thr Tyr
80 85 90
Asn Arg Ala Gln Asp Ile Gln Gly Ile Lys Ile Ile Thr Tyr Cys
95 100 105
Ser Pro Leu Tyr Phe Ala Asn Ser Glu Ile Phe Arg Gln Lys Val
110 115 120
Ile Ala Lys Thr Val Ser Leu Gln Glu Leu Gln Gln Asp Phe Glu
125 130 135
Asn Ala Pro Pro Thr Asp Pro Asn Asn Asn Gln Thr Pro Ala Asn
140 145 150
Gly Thr Ser Val Ser Tyr Ile Thr Phe Ser Pro Asp Ser Ser Ser
155 160 165
Pro Ala Gln Ser Glu Pro Pro Ala Ser Ala Glu Ala Pro Gly Glu
170 175 180
Pro Ser Asp Met Leu Ala Ser Val Pro Pro Phe Val Thr Phe His
185 190 195
Thr Leu Ile Leu Asp Met Ser Gly Val Ser Phe Val Asp Leu Met
200 205 210
Gly Ile Lys Ala Leu Ala Lys Leu Ser Ser Thr Tyr Gly Lys Ile
215 220 225
Gly Val Lys Val Phe Leu Val Asn Ile His Ala Gln Val Tyr Asn
230 235 240
Asp Ile Ser His Gly Gly Val Phe Glu Asp Gly Ser Leu Glu Cys
245 250 255
Lys His Val Phe Pro Ser Ile His Asp Ala Val Leu Phe Ala Gln
260 265 270
Ala Asn Ala Arg Asp Val Thr Pro Gly His Asn Phe Gln Gly Ala
275 280 285
Pro Gly Asp Ala Glu Leu Ser Leu Tyr Asp Ser Glu Glu Asp Ile
290 295 300
Arg Ser Tyr Trp Asp Leu Glu Gln Glu Met Phe Gly Ser Met Phe
305 310 315
His Ala Glu Thr Leu Thr Ala Leu
320

<210> 151
<211> 628
<212> PRT

<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:238218.20.orf1:2002JAN18

<400> 151
Arg Gly Ala Ala Arg Thr Gly Gly Arg Arg Gly Gly Lys Asp Gly
1 5 10 15
Ala Val Thr Ala Gly Pro Glu Pro Ser Arg Pro His Pro Ala Pro
20 25 30
Trp Pro Leu Gly Pro Ala Glu Met Glu Ser Thr Ala Tyr Pro Leu
35 40 45
Asn Leu Ser Leu Lys Glu Glu Glu Glu Glu Glu Glu Ile Gln Ser
50 55 60
Arg Glu Leu Glu Asp Gly Pro Ala Asp Met Gln Lys Val Arg Ile
65 70 75
Cys Ser Glu Gly Gly Trp Val Pro Ala Leu Phe Asp Glu Val Ala
80 85 90
Ile Tyr Phe Ser Asp Glu Glu Trp Glu Val Leu Thr Glu Gln Gln
95 100 105
Lys Ala Leu Tyr Arg Glu Val Met Arg Met Asn Tyr Glu Thr Val
110 115 120
Leu Ser Leu Glu Phe Pro Phe Pro Lys Pro Asp Met Ile Thr Arg
125 130 135
Leu Glu Gly Glu Glu Glu Ser Gln Asn Ser Asp Glu Trp Gln Leu
140 145 150
Gln Gly Gly Thr Ser Ala Glu Asn Glu Glu Ser Asp Val Lys Pro
155 160 165
Pro Asp Trp Pro Asn Pro Met Asn Ala Thr Ser Gln Phe Pro Gln
170 175 180
Pro Gln His Phe Asp Ser Phe Gly Leu Arg Leu Pro Arg Asp Ile
185 190 195
Thr Glu Leu Pro Glu Trp Ser Glu Gly Tyr Pro Phe Tyr Met Ala
200 205 210
Met Gly Phe Pro Gly Tyr Asp Leu Ser Ala Asp Asp Ile Ala Gly
215 220 225
Lys Phe Gln Phe Ser Arg Gly Met Arg Arg Ser Tyr Asp Ala Gly
230 235 240
Phe Lys Leu Met Val Val Glu Tyr Ala Glu Ser Thr Asn Asn Cys
245 250 255
Gln Ala Ala Lys Gln Phe Gly Val Leu Glu Lys Asn Val Arg Asp
260 265 270
Trp Arg Lys Val Lys Pro Gln Leu Gln Asn Ala His Ala Met Arg
275 280 285
Arg Ala Phe Arg Gly Pro Lys Asn Gly Arg Phe Ala Leu Val Asp
290 295 300
Gln Arg Val Ala Glu Tyr Val Arg Tyr Met Gln Ala Lys Gly Asp
305 310 315
Pro Ile Thr Arg Glu Ala Met Gln Leu Lys Ala Leu Glu Ile Ala
320 325 330
Gln Glu Met Asn Ile Pro Glu Lys Gly Phe Lys Ala Ser Leu Gly
335 340 345
Trp Cys Arg Arg Met Met Arg Arg Tyr Asp Leu Ser Leu Arg His
350 355 360
Lys Val Pro Val Pro Gln His Leu Pro Glu Asp Leu Thr Glu Lys
365 370 375
Leu Val Thr Tyr Gln Arg Ser Val Leu Ala Leu Arg Arg Ala His
380 385 390
Asp Tyr Glu Val Ala Gln Met Gly Asn Ala Asp Glu Thr Pro Ile
395 400 405
Cys Leu Glu Val Pro Ser Arg Val Thr Val Asp Asn Gln Gly Glu
410 415 420

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Lys Pro Val Leu Ala Asp Gly Arg Lys Leu Pro Pro Tyr Ile Ile
                425                 430                 435
Leu Arg Gly Thr Tyr Ile Pro Pro Gly Lys Phe Pro Ser Gly Met
                440                 445                 450
Glu Ile Arg Cys His Arg Tyr Gly Trp Met Thr Glu Asp Leu Met
                455                 460                 465
Gln Asp Trp Leu Glu Val Val Trp Arg Arg Arg Thr Gly Ala Val
                470                 475                 480
Pro Lys Gln Arg Gly Met Leu Ile Leu Asn Gly Phe Arg Gly His
                485                 490                 495
Gly Lys Asp Ser Val Lys Asn Ser Met Glu Ser Met Asn Thr Asp
                500                 505                 510
Met Val Ile Ile Pro Gly Gly Leu Thr Ser Gln Leu Gln Val Leu
                515                 520                 525
Asp Val Val Val Tyr Lys Pro Leu Asn Asp Ser Val Arg Ala Gln
                530                 535                 540
Tyr Ser Asn Trp Leu Leu Ala Gly Asn Leu Ala Leu Ser Pro Thr
                545                 550                 555
Gly Asn Ala Lys Lys Pro Pro Leu Gly Leu Phe Leu Glu Trp Val
                560                 565                 570
Met Val Ala Trp Asn Ser Ile Ser Ser Glu Ser Ile Val Gln Gly
                575                 580                 585
Phe Lys Lys Cys His Ile Ser Ser Asn Leu Glu Glu Glu Asp Asp
                590                 595                 600
Val Leu Trp Glu Ile Glu Ser Glu Leu Pro Gly Gly Gly Glu Pro
                605                 610                 615
Pro Lys Asp Cys Asp Thr Glu Ser Met Ala Glu Ser Asn
                620                 625
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<210> 152
<211> 183
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:239939.14.orf3:2002JAN18

<400> 152

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His Arg Lys Asp Gly Val Val Glu Arg Gly Leu Glu Glu Trp Arg
 1               5                  10                  15
Asn Lys Gly Lys Thr Ser Leu Ala His Gln Phe Val Glu Gly Glu
                20                  25                  30
Phe Ser Glu Gly Tyr Asp Pro Thr Val Glu Asn Thr Tyr Ser Lys
                35                  40                  45
Ile Val Thr Leu Gly Lys Asp Glu Phe His Leu His Leu Val Asp
                50                  55                  60
Thr Ala Gly Gln Asp Glu Tyr Ser Ile Leu Pro Tyr Ser Phe Ile
                65                  70                  75
Ile Gly Val His Gly Tyr Val Leu Val Tyr Ser Val Thr Ser Leu
                80                  85                  90
His Ser Phe Gln Val Ile Glu Ser Leu Tyr Gln Lys Leu His Glu
                95                 100                 105
Gly His Gly Lys Thr Arg Val Pro Val Val Leu Val Gly Asn Lys
               110                 115                 120
Ala Asp Leu Ser Pro Glu Arg Glu Val Gln Ala Val Glu Gly Lys
               125                 130                 135
Lys Leu Ala Glu Ser Trp Gly Ala Thr Phe Met Glu Ser Ser Ala
               140                 145                 150
Arg Glu Asn Gln Leu Thr Gln Gly Ile Phe Thr Lys Val Ile Gln
               155                 160                 165
Glu Ile Ala Arg Val Glu Asn Ser Tyr Gly Gln Glu Arg Arg Cys
               170                 175                 180
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His Leu Met

<210> 153
<211> 338
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:242288.11.orf1:2002JAN18

<400> 153
Glu His Val Gly Asp Thr Leu Gln Leu Pro Ala Glu Arg Gln Ala
1 5 10 15
Arg Arg Pro Pro Ala Arg Ala Arg Gln Gly Lys Trp Asp Ala Arg
20 25 30
Lys Gly Pro Leu Ala Pro Ala His His Ser Gly Ser His Ser Glu
35 40 45
Tyr Pro Met Ser Ser Ser Gly Leu Pro Cys Ser Trp Trp Trp Thr
50 55 60
Gln Ala Thr Pro Ala Pro Thr Trp Thr Thr Ser Ser Arg Leu Ala
65 70 75
Arg Ala Pro Arg Ala Ser Cys Ala Ser Pro Pro Cys Ala Ala Arg
80 85 90
Ala Ser Trp Trp Pro Ser Arg Arg Trp Thr Cys Ala Ser Ser Arg
95 100 105
Gly Arg Glu Leu Leu Phe Asn Glu Val Val Ile Met Arg Asp Tyr
110 115 120
Gln His Glu Asn Val Val Glu Met Tyr Asn Ser Tyr Leu Val Gly
125 130 135
Asp Glu Leu Trp Val Val Met Glu Phe Leu Glu Gly Gly Ala Leu
140 145 150
Thr Asp Ile Val Thr His Thr Arg Met Asn Glu Glu Gln Ile Ala
155 160 165
Ala Val Cys Leu Ala Val Leu Gln Ala Leu Ser Val Leu His Ala
170 175 180
Gln Gly Val Ile His Arg Asp Ile Lys Ser Asp Ser Ile Leu Leu
185 190 195
Thr His Asp Gly Arg Val Lys Leu Ser Asp Phe Gly Phe Cys Ala
200 205 210
Gln Val Ser Lys Glu Val Pro Arg Arg Lys Ser Leu Val Gly Thr
215 220 225
Pro Tyr Trp Met Ala Pro Glu Leu Ile Ser Arg Leu Pro Tyr Gly
230 235 240
Pro Glu Val Asp Ile Trp Ser Leu Gly Ile Met Val Ile Glu Met
245 250 255
Val Asp Gly Glu Pro Pro Tyr Phe Asn Glu Pro Pro Leu Lys Ala
260 265 270
Met Lys Met Ile Arg Asp Asn Leu Pro Pro Arg Leu Lys Asn Leu
275 280 285
His Lys Val Ser Pro Ser Leu Lys Gly Phe Leu Asp Arg Leu Leu
290 295 300
Val Arg Asp Pro Ala Gln Arg Ala Thr Ala Ala Glu Leu Leu Lys
305 310 315
His Pro Phe Leu Ala Lys Ala Gly Pro Pro Ala Ser Ile Val Pro
320 325 330
Leu Met Arg Gln Asn Arg Thr Arg
335

<210> 154
<211> 191
<212> PRT

<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:242491.29.orf1:2002JAN18

<400> 154
Gly Ala Met Ala Gly Val Gly Ala Gly Pro Leu Arg Ala Met Gly
1 5 10 15
Arg Gln Ala Leu Leu Leu Leu Ala Leu Cys Ala Thr Gly Ala Gln
20 25 30
Gly Leu Tyr Phe His Ile Gly Glu Thr Glu Lys Arg Cys Phe Ile
35 40 45
Glu Glu Ile Pro Asp Glu Thr Met Val Ile Gly Asn Tyr Arg Thr
50 55 60
Gln Met Trp Asp Lys Gln Lys Glu Val Phe Leu Pro Ser Thr Pro
65 70 75
Gly Leu Gly Met His Val Glu Val Lys Asp Pro Asp Gly Lys Met
80 85 90
Leu Gln Val Val Leu Ser Arg Gln Tyr Gly Ser Glu Gly Arg Phe
95 100 105
Thr Phe Thr Ser His Thr Pro Gly Asp His Gln Ile Cys Leu His
110 115 120
Ser Asn Ser Thr Arg Met Ala Leu Phe Ala Gly Gly Lys Leu Arg
125 130 135
Val His Leu Asp Ile Gln Val Gly Glu His Ala Asn Asn Tyr Pro
140 145 150
Glu Ile Ala Ala Lys Asp Lys Leu Thr Glu Leu Gln Leu Arg Ala
155 160 165
Arg Gln Leu Leu Asp Gln Val Glu Gln Ile Gln Lys Glu Gln Asp
170 175 180
Tyr Gln Arg Ala Ser Ala Tyr Leu Leu Val Ile
185 190

<210> 155
<211> 317
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:243488.41.orf3:2002JAN18

<400> 155
Ala Ala Ala Val Ala Phe Gly Ala Glu Val Gly Val Arg Leu Ala
1 5 10 15
Leu Phe Ala Ala Phe Leu Val Thr Glu Leu Leu Pro Pro Phe Gln
20 25 30
Arg Leu Ile Gln Pro Glu Glu Met Trp Leu Tyr Arg Asn Pro Tyr
35 40 45
Val Glu Ala Glu Tyr Phe Pro Thr Lys Pro Met Phe Lys Ala Asp
50 55 60
Thr Arg Asp Ser Arg Gln Ala Cys Leu Ala Ala Ser Leu Ala Leu
65 70 75
Ala Leu Asn Gly Val Phe Thr Asn Thr Ile Lys Leu Ile Val Gly
80 85 90
Arg Pro Arg Pro Asp Phe Phe Tyr Arg Cys Phe Pro Asp Gly Leu
95 100 105
Ala His Ser Asp Leu Met Cys Thr Gly Asp Lys Asp Val Val Asn
110 115 120
Glu Gly Arg Lys Ser Phe Pro Ser Gly His Ser Ser Phe Ala Phe
125 130 135
Ala Gly Leu Ala Phe Ala Ser Phe Tyr Leu Ala Gly Lys Leu His

140 145 150
Cys Phe Thr Pro Gln Gly Arg Gly Lys Ser Trp Arg Phe Cys Ala
155 160 165
Phe Leu Ser Pro Leu Leu Phe Ala Ala Val Ile Ala Leu Ser Arg
170 175 180
Thr Cys Asp Tyr Lys His His Trp Gln Asp Val Leu Val Gly Ser
185 190 195
Met Ile Gly Met Thr Phe Ala Tyr Val Cys Tyr Arg Gln Tyr Tyr
200 205 210
Pro Pro Leu Thr Asp Ala Glu Cys His Lys Pro Phe Gln Asp Lys
215 220 225
Leu Val Leu Ser Thr Ala Gln Lys Pro Gly Asp Ser Tyr Cys Phe
230 235 240
Asp Asn Leu Lys Ile Glu Ser Gly Arg Ala Trp Trp Leu Met Pro
245 250 255
Val Ile Pro Thr Leu Trp Glu Ala Glu Glu Gly Gly Ser Pro Glu
260 265 270
Val Arg Thr Ser Leu Ala Asn Met Val Asn Pro Val Ser Thr Lys
275 280 285
Asn Thr Lys Ile Ser Gln Glu Leu Cys Ala Val Ile Pro Ala Thr
290 295 300
Trp Glu Ala Glu Val Gly Glu Leu Leu Glu Pro Gly Ser Trp Arg
305 310 315
Phe Gln

<210> 156
<211> 617
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:247792.18.orf2:2002JAN18

<400> 156
Ser Leu Lys Trp Gly Ser Gly Gly Arg Glu Thr Ala Ser Arg Gly
1 5 10 15
Ala Trp Lys Val Val Lys Pro Glu Ser Asn Asp Lys Glu Thr Glu
20 25 30
Ala Ala Tyr Glu Ser Asp Ile Pro Glu Glu Leu Cys Gly His His
35 40 45
Leu Pro Gln Gln Ser Leu Lys Ser Tyr Asn Asp Ser Pro Asp Val
50 55 60
Ile Val Glu Ala Gln Phe Asp Gly Ser Asp Ser Glu Asp Gly His
65 70 75
Gly Ile Thr Gln Asn Val Leu Val Asp Gly Val Lys Lys Leu Ser
80 85 90
Val Cys Val Ser Glu Lys Gly Arg Glu Asp Gly Asp Ala Pro Val
95 100 105
Thr Lys Asp Glu Thr Thr Cys Ile Ser Gln Asp Thr Arg Ala Leu
110 115 120
Ser Glu Lys Ser Leu Gln Arg Ser Ala Lys Val Val Tyr Ile Leu
125 130 135
Glu Lys Lys His Ser Arg Ala Ala Thr Gly Phe Leu Lys Leu Leu
140 145 150
Ala Asp Lys Asn Ser Glu Leu Phe Arg Lys Tyr Ala Leu Phe Ser
155 160 165
Pro Ser Asp His Arg Val Pro Arg Ile Tyr Val Pro Leu Lys Asp
170 175 180
Cys Pro Gln Asp Phe Val Ala Arg Pro Lys Asp Tyr Ala Asn Thr
185 190 195
Leu Phe Ile Cys Arg Ile Val Asp Trp Lys Glu Asp Cys Asn Phe

200 205 210
Ala Leu Gly Gln Leu Ala Lys Ser Leu Gly Gln Ala Gly Glu Ile
215 220 225
Glu Pro Glu Thr Glu Gly Ile Leu Thr Glu Tyr Gly Val Asp Phe
230 235 240
Ser Asp Phe Ser Ser Glu Val Leu Glu Cys Leu Pro Gln Gly Leu
245 250 255
Pro Trp Thr Ile Pro Pro Glu Glu Phe Ser Lys Arg Arg Asp Leu
260 265 270
Arg Lys Asp Cys Ile Phe Thr Ile Asp Pro Ser Thr Ala Arg Asp
275 280 285
Leu Asp Asp Ala Leu Ser Cys Lys Pro Leu Ala Asp Gly Asn Phe
290 295 300
Lys Val Gly Val His Ile Ala Asp Val Ser Tyr Phe Val Pro Glu
305 310 315
Gly Ser Asp Leu Asp Lys Val Ala Ala Glu Arg Ala Thr Ser Val
320 325 330
Tyr Leu Val Gln Lys Val Val Pro Met Leu Pro Arg Leu Leu Cys
335 340 345
Glu Glu Leu Cys Ser Leu Asn Pro Met Ser Asp Lys Leu Thr Phe
350 355 360
Ser Val Ile Trp Thr Leu Thr Pro Glu Gly Lys Ile Leu Asp Glu
365 370 375
Trp Phe Gly Arg Thr Ile Ile Arg Ser Cys Thr Lys Leu Ser Tyr
380 385 390
Glu His Ala Gln Ser Met Ile Glu Ser Pro Thr Glu Lys Ile Pro
395 400 405
Ala Lys Glu Leu Pro Pro Ile Ser Pro Glu His Ser Ser Glu Glu
410 415 420
Val His Gln Ala Val Leu Asn Leu His Gly Ile Ala Lys Gln Leu
425 430 435
Arg Gln Gln Arg Phe Val Asp Gly Ala Leu Arg Leu Asp Gln Leu
440 445 450
Lys Leu Ala Phe Thr Leu Asp His Glu Thr Gly Leu Pro Gln Gly
455 460 465
Cys His Ile Tyr Glu Tyr Arg Glu Ser Asn Lys Leu Val Glu Glu
470 475 480
Phe Met Leu Leu Ala Asn Met Ala Val Ala His Lys Ile His Arg
485 490 495
Ala Phe Pro Glu Gln Ala Leu Leu Arg Arg His Pro Pro Pro Gln
500 505 510
Thr Arg Met Leu Ser Asp Leu Val Glu Phe Cys Asp Gln Met Gly
515 520 525
Leu Pro Val Asp Phe Ser Ser Ala Gly Ala Leu Asn Lys Ser Leu
530 535 540
Thr Gln Thr Phe Gly Asp Asp Lys Tyr Ser Leu Ala Arg Lys Glu
545 550 555
Val Leu Thr Asn Met Cys Ser Arg Pro Met Gln Met Ala Leu Tyr
560 565 570
Phe Cys Ser Gly Leu Leu Gln Asp Pro Ala Gln Phe Arg His Tyr
575 580 585
Ala Leu Asn Val Pro Ser Val His Thr Leu His Leu Ala His Pro
590 595 600
Pro Leu Cys Arg Arg Pro Gly Ala Pro Pro Pro Gly Cys Arg Val
605 610 615
Arg Leu

<210> 157
<211> 371
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:253193.17.orf3:2002JAN18

<400> 157
Tyr Leu Asn Leu Leu Val Thr Ser Trp Arg Met Asn Asp Ser Leu
1 5 10 15
Val Ile Gln Gln Asn Asp Leu Val Phe Glu Phe Ala Ser Asn Val
20 25 30
Met Glu Asp Glu Arg Gln Leu Gly Asp Pro Ala Ile Phe Pro Ala
35 40 45
Val Ile Val Glu His Val Pro Gly Ala Asp Ile Leu Asn Ser Tyr
50 55 60
Ala Gly Leu Ala Cys Val Glu Glu Pro Asn Asp Met Ile Thr Glu
65 70 75
Ser Ser Leu Asp Val Ala Glu Glu Glu Ile Ile Asp Asp Asp Asp
80 85 90
Asp Asp Ile Thr Leu Thr Val Glu Ala Ser Cys His Asp Gly Asp
95 100 105
Glu Thr Ile Glu Thr Ile Glu Ala Ala Glu Ala Leu Leu Asn Met
110 115 120
Asp Ser Pro Gly Pro Met Leu Asp Glu Lys Arg Ile Asn Asn Asn
125 130 135
Ile Phe Ser Ser Pro Glu Asp Asp Met Val Val Ala Pro Val Thr
140 145 150
His Val Ser Val Thr Leu Asp Gly Ile Pro Glu Val Met Glu Thr
155 160 165
Gln Gln Val Gln Glu Lys Tyr Ala Asp Ser Pro Gly Ala Ser Ser
170 175 180
Pro Glu Gln Pro Lys Arg Lys Lys Gly Arg Lys Thr Lys Pro Pro
185 190 195
Arg Pro Asp Ser Pro Ala Thr Thr Pro Asn Ile Ser Val Lys Lys
200 205 210
Lys Asn Lys Asp Gly Lys Gly Asn Thr Ile Tyr Leu Trp Glu Phe
215 220 225
Leu Leu Ala Leu Leu Gln Asp Lys Ala Thr Cys Pro Lys Tyr Ile
230 235 240
Lys Trp Thr Gln Arg Glu Lys Gly Ile Phe Lys Leu Val Asp Ser
245 250 255
Lys Ala Val Ser Arg Leu Trp Gly Lys His Lys Asn Lys Pro Asp
260 265 270
Met Asn Tyr Glu Thr Met Gly Arg Ala Leu Arg Tyr Tyr Tyr Gln
275 280 285
Arg Gly Ile Leu Ala Lys Val Glu Gly Gln Arg Leu Val Tyr Gln
290 295 300
Phe Lys Glu Met Pro Lys Asp Leu Ile Tyr Ile Asn Asp Glu Asp
305 310 315
Pro Ser Ser Ser Ile Glu Ser Ser Asp Pro Ser Leu Ser Ser Ser
320 325 330
Ala Thr Ser Asn Arg Asn Gln Thr Ser Arg Ser Arg Val Ser Ser
335 340 345
Ser Pro Gly Val Lys Gly Gly Ala Thr Thr Val Leu Lys Pro Gly
350 355 360
Asn Ser Lys Ser Cys Lys Ser Gln Arg Ser Cys
365 370

<210> 158
<211> 871
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature

<223> Incyte ID No: LG:257088.20.orf2:2002JAN18

<400> 158
Arg Leu Phe Val Leu Ile Ser Leu Glu Leu Lys Met Leu Tyr Phe
1 5 10 15
Ser Arg Ser His Phe Pro Arg Pro Cys Gly Gly Gln Val Ser Ala
20 25 30
Gly Ser Gly Leu Thr Leu Leu Leu Leu Leu Leu Pro Ala Leu Trp
35 40 45
Arg Gly Trp Leu Glu Gly Asp Gly Gln Gln Ala Val Pro Ala Arg
50 55 60
Gly Glu Pro Gln Gln Asp Cys Cys Val Lys Thr Glu Leu Leu Gly
65 70 75
Glu Glu Thr Pro Met Ala Ala Asp Glu Gly Ser Ala Glu Lys Gln
80 85 90
Ala Gly Glu Ala His Met Ala Ala Asp Gly Glu Thr Asn Gly Ser
95 100 105
Cys Glu Asn Ser Asp Ala Ser Ser His Ala Asn Ala Ala Lys His
110 115 120
Thr Gln Asp Ser Ala Arg Val Asn Pro Gln Asp Gly Thr Asn Thr
125 130 135
Leu Thr Arg Ile Ala Glu Asn Gly Val Ser Glu Arg Asp Ser Glu
140 145 150
Ala Ala Lys Gln Asn His Val Thr Ala Asp Asp Phe Val Gln Thr
155 160 165
Ser Val Ile Gly Ser Asn Gly Tyr Ile Leu Asn Lys Pro Ala Leu
170 175 180
Gln Ala Gln Pro Leu Arg Thr Thr Ser Thr Leu Ala Ser Ser Leu
185 190 195
Pro Gly His Ala Ala Lys Thr Leu Pro Gly Gly Ala Gly Lys Gly
200 205 210
Arg Thr Pro Ser Ala Phe Pro Gln Thr Pro Ala Ala Pro Pro Ala
215 220 225
Thr Leu Gly Glu Gly Ser Ala Asp Thr Glu Asp Arg Lys Leu Pro
230 235 240
Ala Pro Gly Ala Asp Val Lys Val His Arg Ala Arg Lys Thr Met
245 250 255
Pro Lys Ser Val Val Gly Leu His Ala Ala Ser Lys Asp Pro Arg
260 265 270
Glu Val Arg Glu Ala Arg Asp His Lys Glu Pro Lys Glu Glu Ile
275 280 285
Asn Lys Asn Ile Ser Asp Phe Gly Arg Gln Gln Leu Leu Pro Pro
290 295 300
Phe Pro Ser Leu His Gln Ser Leu Pro Gln Asn Gln Cys Tyr Met
305 310 315
Ala Thr Thr Lys Ser Gln Thr Ala Cys Leu Pro Phe Val Leu Ala
320 325 330
Ala Ala Val Ser Arg Lys Lys Lys Arg Arg Met Gly Thr Tyr Ser
335 340 345
Leu Val Pro Lys Lys Lys Thr Lys Val Leu Lys Gln Arg Thr Val
350 355 360
Ile Glu Met Phe Lys Ser Ile Thr His Ser Thr Val Gly Ser Lys
365 370 375
Gly Glu Lys Asp Leu Gly Ala Ser Ser Leu His Val Asn Gly Glu
380 385 390
Ser Leu Glu Met Asp Ser Asp Glu Asp Asp Ser Glu Glu Leu Glu
395 400 405
Glu Asp Asp Gly His Gly Ala Glu Gln Ala Ala Ala Phe Pro Thr
410 415 420
Glu Asp Ser Arg Thr Ser Lys Glu Ser Met Ser Glu Ala Asp Arg
425 430 435
Ala Gln Lys Ser Ser Glu Ser Ser Ile Lys Lys Lys Phe Leu Lys
440 445 450

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Arg Lys Gly Lys Thr Asp Ser Pro Trp Ile Lys Pro Ala Arg Lys
                455                 460                 465
Arg Arg Arg Arg Ser Arg Lys Lys Pro Ser Gly Ala Leu Gly Ser
                470                 475                 480
Glu Ser Tyr Lys Ser Ser Ala Gly Ser Ala Glu Gln Thr Ala Pro
                485                 490                 495
Gly Asp Ser Thr Gly Tyr Met Glu Val Ser Leu Asp Ser Leu Asp
                500                 505                 510
Leu Arg Val Lys Gly Ile Leu Ser Ser Gln Ala Glu Gly Leu Ala
                515                 520                 525
Asn Gly Pro Asp Val Leu Glu Thr Asp Gly Leu Gln Glu Val Pro
                530                 535                 540
Leu Cys Ser Cys Arg Met Glu Thr Pro Lys Ser Arg Glu Ile Thr
                545                 550                 555
Thr Leu Ala Asn Asn Gln Cys Met Ala Thr Glu Ser Val Asp His
                560                 565                 570
Glu Gly Asn Phe Met Glu Cys Gln Pro Glu Ser Ser Ile Ser His
                575                 580                 585
Arg Phe His Lys Asp Cys Ala Ser Arg Val Asn Asn Ala Ser Tyr
                590                 595                 600
Cys Pro His Cys Gly Glu Glu Ser Ser Lys Ala Lys Glu Val Thr
                605                 610                 615
Ile Ala Lys Ala Asp Thr Thr Ser Thr Val Thr Pro Val Pro Gly
                620                 625                 630
Gln Glu Lys Gly Ser Ala Leu Glu Gly Arg Ala Asp Thr Thr Thr
                635                 640                 645
Gly Ser Ala Ala Gly Pro Pro Leu Ser Glu Asp Asp Lys Leu Gln
                650                 655                 660
Gly Ala Ala Ser His Val Pro Glu Gly Phe Asp Pro Thr Gly Pro
                665                 670                 675
Ala Gly Leu Gly Arg Pro Thr Pro Gly Leu Ser Gln Gly Pro Gly
                680                 685                 690
Lys Glu Thr Leu Glu Ser Ala Leu Ile Ala Leu Asp Ser Glu Lys
                695                 700                 705
Pro Lys Lys Leu Arg Phe His Pro Lys Gln Leu Tyr Phe Ser Ala
                710                 715                 720
Arg Gln Gly Glu Leu Gln Lys Val Leu Leu Met Leu Val Asp Gly
                725                 730                 735
Ile Asp Pro Asn Phe Lys Met Glu His Gln Asn Lys Arg Ser Pro
                740                 745                 750
Leu His Ala Ala Ala Glu Ala Gly His Val Asp Ile Cys His Met
                755                 760                 765
Leu Val Gln Ala Gly Ala Asn Ile Asp Thr Cys Ser Glu Asp Gln
                770                 775                 780
Arg Thr Pro Leu Met Glu Ala Ala Glu Asn Asn His Leu Glu Ala
                785                 790                 795
Val Lys Tyr Leu Ile Lys Ala Gly Ala Leu Val Asp Pro Lys Asp
                800                 805                 810
Ala Glu Gly Ser Thr Cys Leu His Leu Ala Ala Lys Lys Gly His
                815                 820                 825
Tyr Glu Val Val Gln Tyr Leu Leu Ser Asn Gly Gln Met Asp Val
                830                 835                 840
Asn Cys Gln Asp Asp Gly Glu Leu Asp Thr His Asp Leu Gly His
                845                 850                 855
Arg Val Gln Ala Arg Gly Pro Arg Glu Ala Ala Ala Val Gln Gly
                860                 865                 870
Leu
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<210> 159
<211> 157
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:265552.1.orf2:2002JAN18

<400> 159
Thr Ile Ala Tyr Leu Leu Ile Lys Ser Lys Cys Leu Ser Leu Ala
1 5 10 15
Val Pro Pro Leu Leu Ser Gly Asn Asp Phe Gln Thr Val Glu Glu
20 25 30
Gly Ser Asn Val Lys Leu Val Cys Asn Val Lys Ala Asn Pro Gln
35 40 45
Ala Gln Met Met Trp Tyr Lys Asn Ser Ser Leu Leu Asp Leu Glu
50 55 60
Lys Ser Arg His Gln Ile Gln Gln Thr Ser Glu Ser Phe Gln Leu
65 70 75
Ser Ile Thr Lys Val Glu Lys Pro Asp Asn Gly Thr Tyr Ser Cys
80 85 90
Ile Ala Lys Ser Ser Leu Lys Thr Glu Ser Leu Asp Phe His Leu
95 100 105
Ile Val Lys Asp Lys Thr Val Gly Val Pro Ile Glu Pro Ile Ile
110 115 120
Ala Ala Cys Val Val Ile Phe Leu Thr Leu Cys Phe Gly Leu Ile
125 130 135
Ala Arg Arg Lys Lys Ile Met Lys Leu Cys Met Lys Asp Lys Asp
140 145 150
Pro His Ser Glu Thr Ala Leu
155

<210> 160
<211> 280
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:275355.12.orf1:2002JAN18

<400> 160
Lys Tyr Glu Phe Asp Asp Tyr Glu Arg Phe Ile Lys Tyr Leu Gly
1 5 10 15
Gly Leu Asn Phe Met Thr Thr Leu Thr Thr His Lys His Leu Pro
20 25 30
His Arg Arg Val Ser Pro Asp Leu Leu Ile Leu Pro Cys Thr Phe
35 40 45
Ala Ser Val Gly Ile Met Trp Ile Asp Ser Val Phe Phe Arg Leu
50 55 60
Val Asp Ala Leu Lys Leu Gln Asp Gln Leu Lys Ala Pro Val Lys
65 70 75
Thr Leu Ser Glu Gly Ile Lys Arg Lys Leu Cys Phe Val Leu Ser
80 85 90
Ile Leu Gly Asn Pro Ser Val Val Leu Leu Asp Glu Pro Ser Thr
95 100 105
Gly Met Asp Pro Glu Gly Gln Gln Gln Met Trp Gln Val Ile Arg
110 115 120
Ala Thr Phe Arg Asn Thr Glu Arg Gly Ala Leu Leu Thr Thr His
125 130 135
Tyr Met Ala Glu Ala Glu Ala Val Cys Asp Arg Val Ala Ile Met
140 145 150
Val Ser Gly Arg Leu Arg Cys Ile Gly Ser Ile Gln His Leu Lys
155 160 165
Ser Lys Phe Gly Lys Asp Tyr Leu Leu Glu Met Lys Leu Lys Asn
170 175 180
Leu Ala Gln Met Glu Pro Leu His Ala Glu Ile Leu Arg Leu Phe

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                185                     190                     195
Pro Gln Ala Ala Gln Gln Glu Arg Phe Ser Ser Leu Met Val Tyr
                200                     205                     210
Lys Leu Pro Val Glu Asp Val Arg Pro Leu Ser Gln Ala Phe Phe
                215                     220                     225
Lys Leu Glu Ile Val Lys Gln Ser Phe Asp Leu Glu Glu Tyr Ser
                230                     235                     240
Leu Ser Gln Ser Thr Leu Glu Gln Val Phe Leu Glu Leu Ser Lys
                245                     250                     255
Glu Gln Glu Leu Gly Asp Leu Glu Glu Asp Phe Asp Pro Ser Val
                260                     265                     270
Lys Trp Lys Leu Leu Leu Gln Glu Glu Pro
                275                     280

<210> 161
<211> 149
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:280014.1.orf1:2002JAN18

<400> 161
Met Trp Ile Val Asp Ser Asn Ile Ile Thr Ala Ile Val Gln Leu
 1              5                       10                      15
His Gly Leu Trp Met Asp Cys Thr Trp Tyr Ser Thr Gly Met Phe
                20                      25                      30
Ser Cys Ala Leu Lys His Ser Ile Leu Ser Leu Pro Ile His Val
                35                      40                      45
Gln Ala Ala Arg Ala Thr Met Val Leu Ala Cys Val Leu Ser Ala
                50                      55                      60
Leu Gly Ile Cys Thr Ser Thr Val Gly Met Lys Cys Thr Arg Leu
                65                      70                      75
Gly Gly Asp Arg Glu Thr Lys Ser His Ala Ser Phe Ala Gly Gly
                80                      85                      90
Val Cys Phe Met Ser Ala Gly Ile Ser Ser Leu Ile Ser Thr Val
                95                      100                     105
Trp Tyr Thr Lys Glu Ile Ile Ala Asn Phe Leu Asp Leu Thr Val
                110                     115                     120
Pro Glu Ser Asn Lys His Glu Pro Gly Gly Ala Ile Tyr Ile Gly
                125                     130                     135
Phe Ile Ser Ala Met Leu Leu Phe Ile Ser Gly Met Ile Phe
                140                     145

<210> 162
<211> 281
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:299937.3.orf3:2002JAN18

<400> 162
Phe Gly Gly Arg Pro Ala Gly Ala Ser Pro Leu Leu Ser Ser Lys
 1              5                       10                      15
Leu Thr Tyr Leu His Leu Pro Ala Gly Ile Lys Met Ala Gly Tyr
                20                      25                      30
Ala Thr Thr Pro Ser Pro Met Gln Thr Leu Gln Glu Glu Ala Val
                35                      40                      45
Cys Ala Ile Cys Leu Asp Tyr Phe Lys Asp Pro Val Ser Ile Ser
                50                      55                      60
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Cys Gly His Asn Phe Cys Arg Gly Cys Val Thr Gln Leu Trp Ser
65 70 75
Lys Glu Asp Glu Glu Asp Gln Asn Glu Glu Glu Asp Glu Trp Glu
80 85 90
Glu Glu Glu Asp Glu Glu Ala Val Gly Ala Met Asp Gly Trp Asp
95 100 105
Gly Ser Ile Arg Glu Val Leu Tyr Arg Gly Asn Ala Asp Glu Glu
110 115 120
Leu Phe Gln Asp Gln Asp Asp Asp Glu Leu Trp Leu Gly Asp Ser
125 130 135
Gly Ile Thr Asn Trp Asp Asn Val Asp Tyr Met Trp Asp Glu Glu
140 145 150
Glu Glu Glu Glu Glu Asp Gln Asp Tyr Tyr Leu Gly Gly Leu Arg
155 160 165
Pro Asp Leu Arg Ile Asp Val Tyr Arg Glu Glu Glu Ile Leu Glu
170 175 180
Ala Tyr Asp Glu Asp Glu Asp Glu Glu Leu Tyr Pro Asp Ile His
185 190 195
Pro Pro Pro Ser Leu Pro Leu Pro Gly Gln Phe Thr Cys Pro Gln
200 205 210
Cys Arg Lys Ser Phe Thr Arg Arg Ser Phe Arg Pro Asn Leu Gln
215 220 225
Leu Ala Asn Met Val Gln Ile Ile Arg Gln Met Cys Pro Thr Pro
230 235 240
Tyr Arg Gly Asn Arg Ser Asn Asp Gln Gly Met Cys Phe Lys His
245 250 255
Gln Glu Ala Leu Lys Leu Phe Cys Glu Val Asp Lys Glu Ala Ile
260 265 270
Cys Val Val Cys Arg Glu Ser Arg Ser His Lys
275 280

<210> 163
<211> 703
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:311197.3.orf3:2002JAN18

<400> 163
Gly Arg Ser Ser Pro Arg Ala Arg Leu Arg Gly Trp Thr Leu Arg
1 5 10 15
Ala Pro Gly Lys Glu Thr Pro Ala Phe Ala Thr Met Leu Ser Ser
20 25 30
Thr Asp Phe Thr Phe Ala Ser Trp Glu Leu Val Val Arg Val Asp
35 40 45
His Pro Asn Glu Glu Gln Gln Lys Asp Val Thr Leu Arg Val Ser
50 55 60
Gly Asp Leu His Val Gly Gly Val Met Leu Lys Leu Val Glu Gln
65 70 75
Ile Asn Ile Ser Gln Asp Trp Ser Asp Phe Ala Leu Trp Trp Glu
80 85 90
Gln Lys His Cys Trp Leu Leu Lys Thr His Trp Thr Leu Asp Lys
95 100 105
Tyr Gly Val Gln Ala Asp Ala Lys Leu Leu Phe Thr Pro Gln His
110 115 120
Lys Met Leu Arg Leu Arg Leu Pro Asn Leu Lys Met Val Arg Leu
125 130 135
Arg Val Ser Phe Ser Ala Val Val Phe Lys Ala Val Ser Asp Ile
140 145 150
Cys Lys Ile Leu Asn Ile Arg Arg Ser Glu Glu Leu Ser Leu Leu
155 160 165

Lys Pro Ser Gly Asp Tyr Phe Lys Lys Lys Lys Lys Lys Asp Lys
170 175 180
Asn Asn Lys Glu Pro Ile Ile Glu Asp Ile Leu Asn Leu Glu Ser
185 190 195
Ser Pro Thr Ala Ser Gly Ser Ser Val Ser Pro Gly Leu Tyr Ser
200 205 210
Lys Thr Met Thr Pro Ile Tyr Asp Pro Ile Asn Gly Thr Pro Ala
215 220 225
Ser Ser Thr Met Thr Trp Phe Ser Asp Ser Pro Leu Thr Glu Gln
230 235 240
Asn Cys Ser Ile Leu Ala Phe Ser Gln Pro Pro Gln Ser Pro Glu
245 250 255
Ala Leu Ala Asp Met Tyr Gln Pro Arg Ser Leu Val Asp Lys Ala
260 265 270
Lys Leu Asn Ala Gly Trp Leu Asp Ser Ser Arg Ser Leu Met Glu
275 280 285
Gln Gly Ile Gln Glu Asp Glu Gln Leu Leu Leu Arg Phe Lys Tyr
290 295 300
Tyr Ser Phe Phe Asp Leu Asn Pro Lys Tyr Asp Ala Val Arg Ile
305 310 315
Asn Gln Leu Tyr Glu Gln Ala Arg Trp Ala Ile Leu Leu Glu Glu
320 325 330
Ile Asp Cys Thr Glu Glu Glu Met Leu Ile Phe Ala Ala Leu Gln
335 340 345
Tyr His Ile Ser Lys Leu Ser Leu Ser Ala Glu Thr Gln Asp Phe
350 355 360
Ala Gly Glu Ser Glu Val Asp Glu Ile Glu Ala Ala Leu Ser Asn
365 370 375
Leu Glu Val Thr Leu Glu Gly Gly Lys Ala Asp Ser Leu Leu Glu
380 385 390
Asp Ile Thr Asp Ile Pro Lys Leu Ala Asp Asn Leu Lys Leu Phe
395 400 405
Arg Pro Lys Lys Leu Leu Pro Lys Ala Phe Lys Gln Tyr Trp Phe
410 415 420
Ile Phe Lys Asp Thr Ser Ile Ala Tyr Phe Lys Asn Lys Glu Leu
425 430 435
Glu Gln Gly Glu Pro Leu Glu Lys Leu Asn Leu Arg Gly Cys Glu
440 445 450
Val Val Pro Asp Val Asn Val Ala Gly Arg Lys Phe Gly Ile Lys
455 460 465
Leu Leu Ile Pro Val Ala Asp Gly Met Asn Glu Met Tyr Leu Arg
470 475 480
Cys Asp His Glu Asn Gln Tyr Ala Gln Trp Met Ala Ala Cys Met
485 490 495
Leu Ala Ser Lys Gly Lys Thr Met Ala Asp Ser Ser Tyr Gln Pro
500 505 510
Glu Val Leu Asn Ile Leu Ser Phe Leu Arg Met Lys Asn Arg Asn
515 520 525
Ser Ala Ser Gln Val Ala Ser Ser Leu Glu Asn Met Asp Met Asn
530 535 540
Pro Glu Cys Phe Val Ser Pro Arg Cys Ala Lys Arg His Lys Ser
545 550 555
Lys Gln Leu Ala Ala Arg Ile Leu Glu Ala His Gln Asn Val Ala
560 565 570
Gln Met Pro Leu Val Glu Ala Lys Leu Arg Phe Ile Gln Ala Trp
575 580 585
Gln Ser Leu Pro Glu Phe Gly Leu Thr Tyr Tyr Leu Val Arg Phe
590 595 600
Lys Gly Ser Lys Lys Asp Asp Ile Leu Gly Val Ser Tyr Asn Arg
605 610 615
Leu Ile Lys Ile Asp Ala Ala Thr Gly Ile Pro Val Thr Thr Trp
620 625 630
Arg Phe Thr Asn Ile Lys Gln Trp Asn Val Asn Trp Glu Thr Arg

```
                635                     640                     645
Gln Val Val Ile Glu Phe Asp Gln Asn Val Phe Thr Ala Phe Thr
                650                     655                     660
Cys Leu Ser Ala Asp Cys Lys Ile Val His Glu Tyr Ile Gly Gly
                665                     670                     675
Tyr Ile Phe Leu Ser Thr Arg Ser Lys Asp Gln Asn Glu Thr Leu
                680                     685                     690
Asp Glu Asp Leu Phe His Lys Leu Thr Gly Gly Gln Asp
                695                     700
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<210> 164
<211> 128
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:321069.2.orf1:2002JAN18

<400> 164

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Gly Thr His Pro Ser Thr Val Leu Leu Ser Pro Leu Ala Gly Val
  1               5                  10                  15
Glu Leu Pro Val Tyr Asp Ile Thr Lys Lys His Leu Ile Leu Ser
                 20                  25                  30
Gly Leu Met Gly Asp Thr Val Tyr Thr His Phe Leu Ser Ser Phe
                 35                  40                  45
Thr Cys Gly Leu Ala Gly Ala Leu Ala Ser Asn Pro Val Asp Val
                 50                  55                  60
Val Arg Thr Arg Met Met Asn Gln Arg Val Leu Arg Asp Gly Arg
                 65                  70                  75
Cys Ser Gly Tyr Thr Gly Thr Leu Asp Cys Leu Leu Gln Thr Trp
                 80                  85                  90
Lys Asn Glu Gly Phe Phe Ala Leu Tyr Lys Gly Phe Trp Pro Asn
                 95                 100                 105
Trp Leu Arg Leu Gly Pro Trp Asn Ile Ile Phe Phe Val Thr Tyr
                110                 115                 120
Glu Gln Leu Lys Lys Leu Asp Leu
                125
```

<210> 165
<211> 1250
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:330900.8.orf2:2002JAN18

<400> 165

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Val Asp Glu His Leu His Glu Asp Asn Gly Glu Val Glu Val Arg
  1               5                  10                  15
Arg Ser Cys Arg Ile Arg Ser Arg Tyr Ser Gly Val Asn Gln Ser
                 20                  25                  30
Met Leu Phe Asp Lys Leu Ile Thr Asn Thr Ala Glu Ala Val Leu
                 35                  40                  45
Gln Lys Met Asp Asp Met Lys Lys Met Arg Arg Gln Arg Met Arg
                 50                  55                  60
Glu Leu Glu Asp Leu Gly Val Phe Asn Glu Thr Glu Glu Ser Asn
                 65                  70                  75
Leu Asn Met Tyr Thr Arg Gly Lys Gln Lys Asp Ile Gln Arg Thr
                 80                  85                  90
Asp Glu Glu Thr Thr Asp Asn Gln Glu Gly Ser Val Glu Ser Ser
                 95                 100                 105
```

Glu Glu Gly Glu Asp Gln Glu His Glu Asp Asp Gly Glu Asp Glu
110 115 120
Asp Asp Glu Asp Asp Asp Asp Asp Asp Asp Asp Asp Asp Asp Asp
125 130 135
Asp Asp Glu Asp Asp Glu Asp Glu Glu Asp Gly Glu Glu Glu Asn
140 145 150
Gln Lys Arg Tyr Tyr Leu Arg Gln Arg Lys Ala Thr Val Tyr Tyr
155 160 165
Gln Ala Pro Leu Glu Lys Pro Arg His Gln Arg Lys Pro Asn Ile
170 175 180
Phe Tyr Ser Gly Pro Ala Ser Pro Ala Arg Pro Arg Tyr Arg Leu
185 190 195
Ser Ser Ala Gly Pro Arg Ser Pro Tyr Cys Lys Arg Met Asn Arg
200 205 210
Arg Arg His Ala Ile His Ser Ser Asp Ser Thr Ser Ser Ser Ser
215 220 225
Ser Glu Asp Glu Gln His Phe Glu Arg Arg Arg Lys Arg Ser Arg
230 235 240
Asn Arg Ala Ile Asn Arg Cys Leu Pro Leu Asn Phe Arg Lys Asp
245 250 255
Glu Leu Lys Gly Ile Tyr Lys Asp Arg Met Lys Ile Gly Ala Ser
260 265 270
Leu Ala Asp Val Asp Pro Met Gln Leu Asp Ser Ser Val Arg Phe
275 280 285
Asp Ser Val Gly Gly Leu Ser Asn His Ile Ala Ala Leu Lys Glu
290 295 300
Met Val Val Phe Pro Leu Leu Tyr Pro Glu Val Phe Glu Lys Phe
305 310 315
Lys Ile Gln Pro Pro Arg Gly Cys Leu Phe Tyr Gly Pro Pro Gly
320 325 330
Thr Gly Lys Thr Leu Val Ala Arg Ala Leu Ala Asn Glu Cys Ser
335 340 345
Gln Gly Asp Lys Arg Val Ala Phe Phe Met Arg Lys Gly Ala Asp
350 355 360
Cys Leu Ser Lys Trp Val Gly Glu Ser Glu Arg Gln Leu Arg Leu
365 370 375
Leu Phe Asp Gln Ala Tyr Gln Met Arg Pro Ser Ile Ile Phe Phe
380 385 390
Asp Glu Ile Asp Gly Leu Ala Pro Val Arg Ser Ser Arg Gln Asp
395 400 405
Gln Ile His Ser Ser Ile Val Ser Thr Leu Leu Ala Leu Met Asp
410 415 420
Gly Leu Asp Ser Arg Gly Glu Ile Val Val Ile Gly Ala Thr Asn
425 430 435
Arg Leu Asp Ser Ile Asp Pro Ala Leu Arg Arg Pro Gly Arg Phe
440 445 450
Asp Arg Glu Phe Leu Phe Ser Leu Pro Asp Lys Glu Ala Arg Lys
455 460 465
Glu Ile Leu Lys Ile His Thr Arg Asp Trp Asn Pro Lys Pro Leu
470 475 480
Asp Thr Phe Leu Glu Glu Leu Ala Glu Asn Cys Val Gly Tyr Cys
485 490 495
Gly Ala Asp Ile Lys Ser Ile Cys Ala Glu Ala Ala Leu Cys Ala
500 505 510
Leu Arg Arg Arg Tyr Pro Gln Ile Tyr Thr Thr Ser Glu Lys Leu
515 520 525
Gln Leu Asp Leu Ser Ser Ile Asn Ile Ser Ala Lys Asp Phe Glu
530 535 540
Val Ala Met Gln Lys Met Ile Pro Ala Ser Gln Arg Ala Val Thr
545 550 555
Ser Pro Gly Gln Ala Leu Ser Thr Val Val Lys Pro Leu Leu Gln
560 565 570
Asn Thr Val Asp Lys Ile Leu Glu Ala Leu Gln Arg Val Phe Pro

575 580 585
His Ala Glu Phe Arg Thr Asn Lys Thr Leu Asp Ser Asp Ile Ser
590 595 600
Cys Pro Leu Leu Glu Ser Asp Leu Ala Tyr Ser Asp Asp Asp Val
605 610 615
Pro Ser Val Tyr Glu Asn Gly Leu Ser Gln Lys Ser Ser His Lys
620 625 630
Ala Lys Asp Asn Phe Asn Phe Leu His Leu Asn Arg Asn Ala Cys
635 640 645
Tyr Gln Pro Met Ser Phe Arg Pro Arg Ile Leu Ile Val Gly Glu
650 655 660
Pro Gly Phe Gly Gln Gly Ser His Leu Ala Pro Ala Val Ile His
665 670 675
Ala Leu Glu Lys Phe Thr Val Tyr Thr Leu Asp Ile Pro Val Leu
680 685 690
Phe Gly Val Ser Thr Thr Ser Pro Glu Glu Thr Cys Ala Gln Val
695 700 705
Ile Arg Glu Ala Lys Arg Thr Ala Pro Ser Ile Val Tyr Val Pro
710 715 720
His Ile His Val Trp Trp Glu Ile Val Gly Pro Thr Leu Lys Ala
725 730 735
Thr Phe Thr Thr Leu Leu Gln Asn Ile Pro Ser Phe Ala Pro Val
740 745 750
Leu Leu Leu Ala Thr Ser Asp Lys Pro His Ser Ala Leu Pro Glu
755 760 765
Glu Val Gln Glu Leu Phe Ile Arg Asp Tyr Gly Glu Ile Phe Asn
770 775 780
Val Gln Leu Pro Asp Lys Glu Glu Arg Thr Lys Phe Phe Glu Asp
785 790 795
Leu Ile Leu Lys Gln Ala Ala Lys Pro Pro Ile Ser Lys Lys Lys
800 805 810
Ala Val Leu Gln Ala Leu Glu Val Leu Pro Val Ala Pro Pro Pro
815 820 825
Glu Pro Arg Ser Leu Thr Ala Glu Glu Val Lys Arg Leu Glu Glu
830 835 840
Gln Glu Glu Asp Thr Phe Arg Glu Leu Arg Ile Phe Leu Arg Asn
845 850 855
Val Thr His Arg Leu Ala Ile Asp Lys Arg Phe Arg Val Phe Thr
860 865 870
Lys Pro Val Asp Pro Asp Glu Val Pro Asp Tyr Val Thr Val Ile
875 880 885
Lys Gln Pro Met Asp Leu Ser Ser Val Ile Ser Lys Ile Asp Leu
890 895 900
His Lys Tyr Leu Thr Val Lys Asp Tyr Leu Arg Asp Ile Asp Leu
905 910 915
Ile Cys Ser Asn Ala Leu Glu Tyr Asn Pro Asp Arg Asp Pro Gly
920 925 930
Asp Arg Leu Ile Arg His Arg Ala Cys Ala Leu Arg Asp Thr Ala
935 940 945
Tyr Ala Ile Ile Lys Glu Glu Leu Asp Glu Asp Phe Glu Gln Leu
950 955 960
Cys Glu Glu Ile Gln Glu Ser Arg Lys Lys Arg Gly Cys Ser Ser
965 970 975
Ser Lys Tyr Ala Pro Ser Tyr Tyr His Val Met Pro Lys Gln Asn
980 985 990
Ser Thr Leu Val Gly Asp Lys Arg Ser Asp Pro Glu Gln Asn Glu
995 1000 1005
Lys Leu Lys Thr Pro Ser Thr Pro Val Ala Cys Ser Thr Pro Ala
1010 1015 1020
Gln Leu Lys Arg Lys Ile Arg Lys Lys Ser Asn Trp Tyr Leu Gly
1025 1030 1035
Thr Ile Lys Lys Arg Arg Lys Ile Ser Gln Ala Lys Asp Asp Ser
1040 1045 1050

Gln Asn Ala Ile Asp His Lys Ile Glu Ser Asp Thr Glu Glu Thr
1055 1060 1065
Gln Asp Thr Ser Val Asp His Asn Glu Thr Gly Asn Thr Gly Glu
1070 1075 1080
Ser Ser Val Glu Glu Asn Glu Lys Gln Gln Asn Ala Ser Glu Ser
1085 1090 1095
Lys Leu Glu Leu Arg Asn Asn Ser Asn Thr Cys Asn Ile Glu Asn
1100 1105 1110
Glu Leu Glu Asp Ser Arg Lys Thr Thr Ala Cys Thr Glu Leu Arg
1115 1120 1125
Asp Lys Ile Ala Cys Asn Gly Asp Ala Ser Ser Ser Gln Ile Ile
1130 1135 1140
His Ile Ser Asp Glu Asn Glu Gly Lys Glu Met Cys Val Leu Arg
1145 1150 1155
Met Thr Arg Ala Arg Arg Ser Gln Val Glu Gln Gln Gln Leu Ile
1160 1165 1170
Thr Val Glu Lys Ala Leu Ala Ile Leu Ser Gln Pro Thr Pro Ser
1175 1180 1185
Leu Val Val Asp His Glu Arg Leu Lys Asn Leu Leu Lys Thr Val
1190 1195 1200
Val Lys Lys Ser Gln Asn Tyr Asn Ile Phe Gln Leu Glu Asn Leu
1205 1210 1215
Tyr Ala Val Ile Ser Gln Cys Ile Tyr Arg His Arg Lys Asp His
1220 1225 1230
Asp Lys Thr Ser Leu Ile Gln Lys Met Glu Gln Glu Val Glu Asn
1235 1240 1245
Phe Ser Cys Ser Arg
1250

<210> 166
<211> 705
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:330931.9.orf1:2002JAN18

<400> 166
Pro Ile Cys Gly Leu Val Ile Lys Arg Lys Ser Tyr Trp Lys Arg
1 5 10 15
His Met Val Ile His Thr Gly Leu Lys Ser His Gln Cys Pro Leu
20 25 30
Cys Pro Phe Arg Cys Ala Arg Lys Asp Asn Leu Lys Ser His Met
35 40 45
Lys Val His Gln His Gln Asp Arg Gly Glu Thr Phe Gln Cys Gln
50 55 60
Leu Cys Pro Phe Thr Ser Ser Arg His Phe Ser Leu Lys Leu His
65 70 75
Met Arg Cys His Gln His Phe Leu Arg Thr Glu Ala Lys Val Lys
80 85 90
Glu Glu Ile Pro Asp Pro Asp Val Lys Gly Ser Pro His Leu Ser
95 100 105
Asp Ser Ala Cys Leu Gly Gln Gln Arg Glu Gly Gly Gly Thr Glu
110 115 120
Leu Val Gly Thr Met Met Thr Ser Asn Thr Pro Glu Arg Thr Ser
125 130 135
Gln Gly Gly Ala Gly Val Ser Pro Leu Leu Val Lys Glu Glu Pro
140 145 150
Lys Glu Asp Asn Gly Leu Pro Thr Ser Phe Thr Leu Asn Ala Ala
155 160 165
Asp Arg Pro Ala Asn His Thr Lys Leu Lys Asp Pro Ser Glu Tyr
170 175 180

Val Ala Asn Ser Ala Ser Ala Leu Phe Ser Gln Asp Ile Ser Val
185 190 195
Lys Met Ala Ser Asp Phe Leu Met Lys Leu Ser Ala Ala Asn Gln
200 205 210
Lys Glu Pro Met Asn Leu Asn Phe Lys Val Lys Glu Glu Pro Lys
215 220 225
Glu Gly Glu Ser Leu Ser Thr Thr Leu Pro Arg Ser Ser Tyr Val
230 235 240
Phe Ser Pro Glu Ser Glu Val Ser Ala Pro Gly Val Ser Glu Asp
245 250 255
Ala Leu Lys Pro Gln Glu Gly Lys Gly Ser Val Leu Arg Arg Asp
260 265 270
Val Ser Val Lys Ala Ala Ser Glu Leu Leu Met Lys Leu Ser Ala
275 280 285
Glu Ser Tyr Lys Glu Thr Gln Met Val Lys Ile Lys Glu Glu Pro
290 295 300
Met Glu Val Asp Ile Gln Asp Ser His Val Ser Ile Ser Pro Ser
305 310 315
Arg Asn Val Gly Tyr Ser Thr Leu Ile Gly Arg Glu Lys Thr Glu
320 325 330
Pro Leu Gln Lys Met Pro Glu Gly Arg Val Pro Pro Glu Arg Asn
335 340 345
Leu Phe Ser Gln Asp Ile Ser Val Lys Met Ala Ser Glu Leu Leu
350 355 360
Phe Gln Leu Ser Glu Lys Val Ser Lys Glu His Asn His Thr Lys
365 370 375
Glu Asn Thr Ile Arg Thr Thr Thr Ser Pro Phe Phe Ser Glu Asp
380 385 390
Thr Phe Arg Gln Ser Pro Phe Thr Ser Asn Ser Lys Glu Leu Leu
395 400 405
Pro Ser Asp Ser Val Leu His Gly Arg Ile Ser Ala Pro Glu Thr
410 415 420
Glu Lys Ile Val Leu Glu Ala Gly Asn Gly Leu Pro Ser Trp Lys
425 430 435
Phe Asn Asp Gln Leu Phe Pro Cys Asp Val Cys Gly Lys Val Phe
440 445 450
Gly Arg Gln Gln Thr Leu Ser Arg His Leu Ser Leu His Thr Glu
455 460 465
Glu Arg Lys Tyr Lys Cys His Leu Cys Pro Tyr Ala Ala Lys Cys
470 475 480
Arg Ala Asn Leu Asn Gln His Leu Thr Val His Ser Val Lys Leu
485 490 495
Val Ser Thr Asp Thr Glu Asp Ile Val Ser Ala Val Thr Ser Glu
500 505 510
Gly Ser Asp Gly Lys Lys His Pro Tyr Tyr Tyr Ser Cys His Val
515 520 525
Cys Gly Phe Glu Thr Glu Leu Asn Val Gln Phe Val Ser His Met
530 535 540
Ser Leu His Val Asp Lys Glu Gln Trp Met Phe Ser Ile Cys Cys
545 550 555
Thr Ala Cys Asp Phe Val Thr Met Glu Glu Ala Glu Ile Lys Thr
560 565 570
His Ile Gly Thr Lys His Thr Gly Glu Asp Arg Lys Thr Pro Ser
575 580 585
Glu Ser Asn Ser Pro Ser Ser Ser Ser Leu Ser Ala Leu Ser Asp
590 595 600
Ser Ala Asn Ser Lys Asp Asp Ser Asp Gly Ser Gln Lys Asn Lys
605 610 615
Gly Gly Asn Asn Leu Leu Val Ile Ser Val Met Pro Gly Ser Gln
620 625 630
Pro Ser Leu Asn Ser Glu Glu Lys Pro Glu Lys Gly Phe Glu Cys
635 640 645
Val Phe Cys Asn Phe Val Cys Lys Thr Lys Asn Met Phe Glu Arg

```
                650                         655                         660
His Leu Gln Ile His Leu Ile Thr Arg Met Phe Glu Cys Asp Val
                665                         670                         675
Cys His Lys Phe Met Lys Thr Pro Glu Gln Leu Leu Glu His Lys
                680                         685                         690
Lys Cys His Thr Val Pro Thr Gly Gly Leu Asn Ser Gly Gln Trp
                695                         700                         705
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<210> 167
<211> 630
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:330985.1.orf3:2002JAN18

<400> 167

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Ser Pro Gly Val Arg Val Arg Gly Ala Gly Ser Gly Ser Pro Arg
  1             5                   10                  15
Ala Ala Ala Pro Pro Ser Arg Arg His Ser Val Thr Phe Val Pro
                20                  25                  30
Ser Gly Ala Ala Arg Gly Leu Ser Arg Met Val Pro Ser Ser Pro
                35                  40                  45
Ala Val Glu Lys Gln Val Pro Val Glu Pro Gly Pro Asp Pro Glu
                50                  55                  60
Leu Arg Ser Trp Arg Arg Leu Val Cys Tyr Leu Cys Phe Tyr Gly
                65                  70                  75
Phe Met Ala Gln Ile Arg Pro Gly Glu Ser Phe Ile Thr Pro Tyr
                80                  85                  90
Leu Leu Gly Pro Asp Lys Asn Phe Thr Arg Glu Gln Val Thr Asn
                95                  100                 105
Glu Ile Thr Pro Val Leu Ser Tyr Ser Tyr Leu Ala Val Leu Val
                110                 115                 120
Pro Val Phe Leu Leu Thr Asp Tyr Leu Arg Tyr Thr Pro Val Leu
                125                 130                 135
Leu Leu Gln Gly Leu Ser Phe Val Ser Val Trp Leu Leu Leu Leu
                140                 145                 150
Leu Gly His Ser Val Ala His Met Gln Leu Met Glu Leu Phe Tyr
                155                 160                 165
Ser Val Thr Met Ala Ala Arg Ile Ala Tyr Ser Ser Tyr Ile Phe
                170                 175                 180
Ser Leu Val Arg Pro Ala Arg Tyr Gln Arg Val Ala Gly Tyr Ser
                185                 190                 195
Arg Ala Ala Val Leu Leu Gly Val Phe Thr Ser Ser Val Leu Gly
                200                 205                 210
Gln Leu Leu Val Thr Val Gly Arg Val Ser Phe Ser Thr Leu Asn
                215                 220                 225
Tyr Ile Ser Leu Ala Phe Leu Thr Phe Ser Val Val Leu Ala Leu
                230                 235                 240
Phe Leu Lys Arg Pro Lys Arg Ser Leu Phe Phe Asn Arg Asp Asp
                245                 250                 255
Arg Gly Arg Cys Glu Thr Ser Ala Ser Glu Leu Glu Arg Met Asn
                260                 265                 270
Pro Gly Pro Gly Gly Lys Leu Gly His Ala Leu Arg Val Ala Cys
                275                 280                 285
Gly Asp Ser Val Leu Ala Arg Met Leu Arg Glu Leu Gly Asp Ser
                290                 295                 300
Leu Arg Arg Pro Gln Leu Arg Leu Trp Ser Leu Trp Trp Val Phe
                305                 310                 315
Asn Ser Ala Gly Tyr Tyr Leu Val Val Tyr Tyr Val His Ile Leu
                320                 325                 330
```

Trp Asn Glu Val Asp Pro Thr Thr Asn Ser Ala Arg Val Tyr Asn
335 340 345
Gly Ala Ala Asp Ala Ala Ser Thr Leu Leu Gly Ala Ile Thr Ser
350 355 360
Phe Ala Ala Gly Phe Val Lys Ile Arg Trp Ala Arg Trp Ser Lys
365 370 375
Leu Leu Ile Ala Gly Val Thr Ala Thr Gln Ala Gly Leu Val Phe
380 385 390
Leu Leu Ala His Thr Arg His Pro Ser Ser Ile Trp Leu Cys Tyr
395 400 405
Ala Ala Phe Val Leu Phe Arg Gly Ser Tyr Gln Phe Leu Val Pro
410 415 420
Ile Ala Thr Phe Gln Ile Ala Ser Ser Leu Ser Lys Glu Leu Cys
425 430 435
Ala Leu Val Phe Gly Val Asn Thr Phe Phe Ala Thr Ile Val Lys
440 445 450
Thr Ile Ile Thr Phe Ile Val Ser Asp Val Arg Gly Leu Gly Leu
455 460 465
Pro Val Arg Lys Gln Phe Gln Leu Tyr Ser Val Tyr Phe Leu Ile
470 475 480
Leu Ser Ile Ile Tyr Phe Leu Gly Ala Met Leu Asp Gly Leu Arg
485 490 495
His Cys Gln Arg Gly His His Pro Arg Gln Pro Pro Ala Gln Gly
500 505 510
Leu Arg Ser Ala Ala Glu Glu Lys Ala Ala Gln Ala Leu Ser Val
515 520 525
Gln Asp Lys Gly Leu Gly Gly Leu Gln Pro Ala Gln Ser Pro Pro
530 535 540
Leu Ser Pro Glu Asp Ser Leu Gly Ala Val Gly Pro Ala Ser Leu
545 550 555
Glu Gln Arg Gln Ser Asp Pro Tyr Leu Ala Gln Ala Pro Ala Pro
560 565 570
Gln Ala Ala Glu Phe Leu Ser Pro Val Thr Thr Pro Ser Pro Cys
575 580 585
Thr Leu Cys Ser Ala Gln Ala Ser Gly Pro Glu Ala Ala Asp Glu
590 595 600
Thr Cys Pro Gln Leu Ala Val His Pro Pro Gly Val Ser Lys Leu
605 610 615
Gly Leu Gln Cys Leu Pro Ser Asp Gly Val Gln Asn Val Asn Gln
620 625 630

<210> 168
<211> 389
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:332027.9.orf3:2002JAN18

<400> 168
Arg Met Pro Phe Met Trp Leu Glu Ser Gly Ile Pro Asn Leu Gly
1 5 10 15
Val Trp Pro Asn Arg Ile His Thr Thr Ala Glu Lys Tyr Arg Glu
20 25 30
Tyr Glu Ala Arg Glu Gln Thr Asp Gln Thr Gln Ala Gln Glu Leu
35 40 45
His Arg Ser Gln Asp Arg Asp Phe Glu Thr Met Ala Lys Leu His
50 55 60
Ile Pro Val Met Val Asp Glu Val Val His Cys Leu Ser Pro Gln
65 70 75
Lys Gly Gln Ile Phe Leu Asp Met Thr Phe Gly Ser Gly Gly His

80 85 90
Thr Lys Ala Ile Leu Gln Lys Glu Ser Asp Ile Val Leu Tyr Ala
95 100 105
Leu Asp Arg Asp Pro Thr Ala Tyr Ala Leu Ala Glu His Leu Ser
110 115 120
Glu Leu Tyr Pro Lys Gln Ile Arg Ala Met Leu Gly Gln Phe Ser
125 130 135
Gln Ala Glu Ala Leu Leu Met Lys Ala Gly Val Gln Pro Gly Thr
140 145 150
Phe Asp Gly Val Leu Met Asp Leu Gly Cys Ser Ser Met Gln Leu
155 160 165
Asp Thr Pro Glu Arg Gly Phe Ser Leu Arg Lys Asp Gly Pro Leu
170 175 180
Asp Met Arg Met Asp Gly Gly Arg Tyr Pro Asp Met Pro Thr Ala
185 190 195
Ala Asp Val Val Asn Ala Leu Asp Gln Gln Ala Leu Ala Ser Ile
200 205 210
Leu Arg Thr Tyr Gly Glu Glu Lys His Ala Lys Lys Ile Ala Ser
215 220 225
Ala Ile Val Gln Ala Arg Ser Ile Tyr Pro Ile Thr Arg Thr Gln
230 235 240
Gln Leu Ala Ser Ile Val Ala Gly Ala Phe Pro Pro Ser Ala Ile
245 250 255
Tyr Thr Arg Lys Asp Leu Leu Gln Arg Ser Thr His Ile Ala Thr
260 265 270
Lys Thr Phe Gln Ala Leu Arg Ile Phe Val Asn Asn Glu Leu Asn
275 280 285
Glu Leu Tyr Thr Gly Leu Lys Thr Ala Gln Lys Phe Leu Arg Pro
290 295 300
Gly Gly Arg Leu Val Ala Leu Ser Phe His Ser Leu Glu Asp Arg
305 310 315
Ile Val Lys Arg Phe Leu Leu Gly Ile Ser Met Thr Glu Arg Phe
320 325 330
Asn Leu Ser Val Arg Gln Gln Val Met Lys Thr Ser Gln Leu Gly
335 340 345
Ser Asp His Glu Asn Thr Glu Glu Val Ser Met Arg Arg Ala Pro
350 355 360
Leu Met Trp Glu Leu Ile His Lys Lys Val Leu Ser Pro Gln Asp
365 370 375
Gln Asp Val Gln Asp Asn Pro Gln Arg Ala Leu Ser Gln Ala
380 385

<210> 169
<211> 381
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:335377.8.orf2:2002JAN18

<400> 169
Arg Glu Ala Val Gln Asp Gly Cys Thr Leu Pro Ala Pro Arg Ser
1 5 10 15
Ser Gly Cys Ser Leu Gln Leu Ser Pro Glu Ser Leu Lys Arg Glu
20 25 30
Pro Ala Ser Cys Leu Pro Gly Ala Met Glu Ala Val Glu Leu Ala
35 40 45
Arg Lys Leu Gln Glu Glu Ala Thr Cys Ser Ile Cys Leu Asp Tyr
50 55 60
Phe Thr Asp Pro Val Met Thr Thr Cys Gly His Asn Phe Cys Arg
65 70 75
Ala Cys Ile Gln Leu Ser Trp Glu Lys Ala Arg Gly Lys Lys Gly

80 85 90
Arg Arg Lys Arg Lys Gly Ser Phe Pro Cys Pro Glu Cys Arg Glu
95 100 105
Met Ser Pro Gln Arg Asn Leu Leu Pro Asn Arg Leu Leu Thr Lys
110 115 120
Val Ala Glu Met Ala Gln Gln His Pro Gly Leu Gln Lys Gln Asp
125 130 135
Leu Cys Gln Glu His His Glu Pro Leu Lys Leu Phe Cys Gln Lys
140 145 150
Asp Gln Ser Pro Ile Cys Val Val Cys Arg Glu Ser Arg Glu His
155 160 165
Arg Leu His Arg Val Leu Pro Ala Glu Glu Ala Val Gln Gly Tyr
170 175 180
Lys Leu Lys Leu Glu Glu Asp Met Glu Tyr Leu Arg Glu Gln Ile
185 190 195
Thr Arg Thr Gly Asn Leu Gln Ala Arg Glu Glu Gln Ser Leu Ala
200 205 210
Glu Trp Gln Gly Lys Val Asn Gly Ala Glu Arg Thr His Cys Ala
215 220 225
Gly Val Glu Lys Met Asn Leu Tyr Leu Val Glu Glu Glu Gln Arg
230 235 240
Leu Leu Gln Ala Leu Glu Thr Glu Glu Glu Glu Thr Ala Ser Arg
245 250 255
Leu Arg Glu Ser Val Ala Cys Leu Asp Arg Gln Gly His Ser Leu
260 265 270
Glu Leu Leu Leu Leu Gln Leu Glu Glu Arg Ser Thr Gln Gly Pro
275 280 285
Leu Gln Met Leu Gln Asp Met Lys Glu Pro Leu Ser Arg Lys Asn
290 295 300
Asn Val Ser Val Gln Cys Pro Glu Val Ala Pro Pro Thr Arg Pro
305 310 315
Arg Thr Val Cys Arg Val Pro Gly Gln Ile Glu Val Leu Arg Gly
320 325 330
Phe Leu Gly Lys Trp Ala Pro Arg Ala Arg Thr Ser Asp Pro Gly
335 340 345
Ser Leu Gly Asp Ala Pro Leu Tyr Pro Leu Ala Ser Glu Ala Thr
350 355 360
Asn Gly Gly Gly Ser Thr Ser Ala Leu Pro Gly Asp Gly His Trp
365 370 375
Leu Phe Thr Val Pro Ser
380

<210> 170
<211> 659
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:337452.25.orf3:2002JAN18

<400> 170
Ile Ser Ile His Pro Leu Cys Phe Ala Leu Glu Leu Ala Pro Leu
1 5 10 15
Ser Ser Leu Asn Thr Val Leu Ser Glu Asn Ala Arg Asp Ser Ser
20 25 30
Phe Ile Pro Leu Gly His Met Leu Thr Gln Lys Ile Ala Tyr Gln
35 40 45
Ile Ala Ser Gly Leu Ala Tyr Leu His Lys Lys Asn Ile Ile Phe
50 55 60
Cys Asp Leu Lys Ser Asp Asn Ile Leu Val Trp Ser Leu Asp Val
65 70 75
Lys Glu His Ile Asn Ile Lys Leu Ser Asp Tyr Gly Ile Ser Arg

80 85 90
Gln Ser Phe His Glu Gly Ala Leu Gly Val Glu Gly Thr Pro Gly
95 100 105
Tyr Gln Ala Pro Glu Ile Arg Pro Arg Ile Val Tyr Asp Glu Lys
110 115 120
Val Asp Met Phe Ser Tyr Gly Met Val Leu Tyr Glu Leu Leu Ser
125 130 135
Gly Gln Arg Pro Ala Leu Gly His His Gln Leu Gln Ile Ala Lys
140 145 150
Lys Leu Ser Lys Gly Ile Arg Pro Val Leu Gly Gln Pro Glu Glu
155 160 165
Val Gln Phe Arg Arg Leu Gln Ala Leu Met Met Glu Cys Trp Asp
170 175 180
Thr Lys Pro Glu Lys Arg Pro Leu Ala Leu Ser Val Val Ser Gln
185 190 195
Met Lys Asp Pro Thr Phe Ala Thr Phe Met Tyr Glu Leu Cys Cys
200 205 210
Gly Lys Gln Thr Ala Phe Phe Ser Ser Gln Gly Gln Glu Tyr Thr
215 220 225
Val Val Phe Trp Asp Gly Lys Glu Glu Ser Arg Asn Tyr Thr Val
230 235 240
Val Asn Thr Glu Lys Gly Leu Met Glu Val Gln Arg Met Cys Cys
245 250 255
Pro Gly Met Lys Val Ser Cys Gln Leu Gln Val Gln Arg Ser Leu
260 265 270
Trp Thr Ala Thr Glu Asp Gln Lys Ile Tyr Ile Tyr Thr Leu Lys
275 280 285
Gly Met Cys Pro Leu Asn Thr Pro Gln Gln Ala Leu Asp Thr Pro
290 295 300
Ala Val Val Thr Cys Phe Leu Ala Val Pro Val Ile Lys Lys Asn
305 310 315
Ser Tyr Leu Val Leu Ala Gly Leu Ala Asp Gly Leu Val Ala Val
320 325 330
Phe Pro Val Val Arg Gly Thr Pro Lys Asp Ser Cys Ser Tyr Leu
335 340 345
Cys Ser His Thr Ala Asn Arg Ser Lys Phe Ser Ile Ala Asp Glu
350 355 360
Asp Ala Arg Gln Asn Pro Tyr Pro Val Lys Ala Met Glu Val Val
365 370 375
Asn Ser Gly Ser Glu Val Trp Tyr Ser Asn Gly Pro Gly Leu Leu
380 385 390
Val Ile Asp Cys Ala Ser Leu Glu Ile Cys Arg Arg Leu Glu Pro
395 400 405
Tyr Met Ala Pro Ser Met Val Thr Ser Val Val Cys Ser Ser Glu
410 415 420
Gly Arg Gly Glu Glu Val Val Trp Cys Leu Asp Asp Lys Ala Asn
425 430 435
Ser Leu Val Met Tyr His Ser Thr Thr Tyr Gln Leu Cys Ala Arg
440 445 450
Tyr Phe Cys Gly Val Pro Ser Pro Leu Arg Asp Met Phe Pro Val
455 460 465
Arg Pro Leu Asp Thr Glu Pro Pro Ala Ala Ser His Thr Ala Asn
470 475 480
Pro Lys Val Pro Glu Gly Asp Ser Ile Ala Asp Val Ser Ile Met
485 490 495
Tyr Ser Glu Glu Leu Gly Thr Gln Ile Leu Ile His Gln Glu Ser
500 505 510
Leu Thr Asp Tyr Cys Ser Met Ser Ser Tyr Ser Ser Ser Pro Pro
515 520 525
Arg Gln Ala Ala Arg Ser Pro Ser Ser Leu Pro Ser Ser Pro Ala
530 535 540
Ser Ser Ser Ser Val Pro Phe Ser Thr Asp Cys Glu Asp Ser Asp
545 550 555

Met Leu His Met Pro Gly Ala Ala Ser Asp Arg Ser Glu His Asp
560 565 570
Leu Thr Pro Met Asp Gly Glu Thr Phe Ser Gln His Leu Gln Ala
575 580 585
Val Lys Ile Leu Ala Val Arg Asp Leu Ile Trp Val Pro Arg Arg
590 595 600
Gly Gly Asp Val Ile Val Ile Gly Leu Glu Lys Asp Ser Glu Ala
605 610 615
Gln Arg Gly Arg Val Ile Ala Val Leu Lys Ala Arg Glu Leu Thr
620 625 630
Pro His Gly Ile Met Pro Val Ser Ser Val Lys Val Cys Trp Ala
635 640 645
Gly Trp Pro Val Arg Asp Met Val Tyr Met Ala Ala Val Met
650 655

<210> 171
<211> 219
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:340580.16.orf2:2002JAN18

<400> 171
Ile Lys His Ser Met Phe Phe Ser Phe Ser Leu Leu Leu Leu Leu
1 5 10 15
Ser Phe Gly Ile Phe Asn Leu Lys Cys Phe Pro Leu Val Val Gly
20 25 30
Phe Ile Leu Pro Leu Pro Leu Pro Phe Ser Tyr Tyr Ser Glu Tyr
35 40 45
Lys Pro Ala Lys Leu Ser Gln Ile Arg Gln Ile Tyr His Thr Glu
50 55 60
Leu Glu Lys Tyr Glu Gln Ala Cys Asn Glu Phe Thr Thr Leu Val
65 70 75
Met Asn Leu Leu Arg Glu Gln Ser Arg Thr Arg Pro Ile Ser Pro
80 85 90
Lys Glu Ile Glu Arg Met Val Ser Ile Ile His Arg Lys Phe Ser
95 100 105
Ser Ile Gln Met Gln Leu Lys Gln Ser Thr Cys Glu Ala Val Met
110 115 120
Ile Leu Arg Ser Arg Phe Leu Asp Ala Arg Arg Lys Arg Arg Asn
125 130 135
Phe Asn Lys Gln Ala Thr Glu Ile Leu Asn Glu Tyr Phe Tyr Ser
140 145 150
His Leu Ser Asn Pro Tyr Pro Ser Glu Glu Ala Lys Glu Glu Leu
155 160 165
Ala Lys Lys Cys Gly Ile Thr Val Ser Gln Val Ser Asn Trp Phe
170 175 180
Gly Asn Lys Arg Ile Arg Tyr Lys Lys Asn Ile Gly Lys Phe Gln
185 190 195
Glu Glu Ala Asn Ile Tyr Cys Cys Gln Asn Ser Cys His Cys Tyr
200 205 210
Gln Cys Val Ser Pro Trp Lys Pro Ser
215

<210> 172
<211> 438
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature

<223> Incyte ID No: LG:350272.6.orf2:2002JAN18

<400> 172
Arg Pro Arg Ala Val Gly His Gly Gly Pro Gly Pro Gly Leu Arg
1 5 10 15
Arg Ser Arg Val Ala Gly Arg Gly Arg Pro Arg Leu His His Leu
20 25 30
Pro Gly Leu Leu Asp Trp Pro Ala Thr Leu Pro Cys Gly His Ser
35 40 45
Phe Cys Arg His Cys Leu Glu Ala Leu Trp Gly Ala Arg Asp Ala
50 55 60
Arg Arg Trp Ala Cys Pro Thr Cys Arg Gln Gly Ala Ala Gln Gln
65 70 75
Pro His Leu Arg Lys Asn Thr Leu Leu Gln Asp Leu Ala Asp Lys
80 85 90
Tyr Arg Arg Ala Ala Arg Glu Ile Gln Ala Gly Ser Asp Pro Ala
95 100 105
His Cys Pro Cys Pro Gly Ser Ser Ser Leu Ser Ser Ala Ala Ala
110 115 120
Arg Pro Arg Arg Arg Pro Glu Leu Gln Arg Val Ala Val Glu Lys
125 130 135
Ser Ile Thr Glu Val Ala Gln Glu Leu Thr Glu Leu Val Glu His
140 145 150
Leu Val Asp Ile Val Arg Ser Leu Gln Asn Gln Arg Pro Leu Ser
155 160 165
Glu Ser Gly Pro Asp Asn Glu Leu Ser Ile Leu Gly Lys Ala Phe
170 175 180
Ser Ser Gly Val Asp Leu Ser Met Ala Ser Pro Lys Leu Val Thr
185 190 195
Ser Asp Thr Ala Ala Gly Lys Ile Arg Asp Ile Leu His Asp Leu
200 205 210
Glu Glu Ile Gln Glu Lys Leu Gln Glu Ser Val Thr Trp Lys Glu
215 220 225
Ala Pro Glu Ala Gln Met Gln Gly Glu Leu Leu Glu Ala Pro Ser
230 235 240
Ser Ser Ser Cys Pro Leu Pro Asp Gln Ser His Pro Ala Leu Arg
245 250 255
Arg Ala Ser Arg Phe Ala Gln Trp Ala Ile His Pro Thr Phe Asn
260 265 270
Leu Lys Ser Leu Ser Cys Ser Leu Glu Val Ser Lys Asp Ser Arg
275 280 285
Thr Val Thr Val Ser His Arg Pro Gln Pro Tyr Arg Trp Ser Cys
290 295 300
Glu Arg Phe Ser Thr Ser Gln Val Leu Cys Ser Gln Ala Leu Ser
305 310 315
Ser Gly Lys His Tyr Trp Glu Val Asp Thr Arg Asn Cys Ser His
320 325 330
Trp Ala Val Gly Val Ala Ser Trp Glu Met Ser Arg Asp Gln Val
335 340 345
Leu Gly Arg Thr Met Asp Ser Cys Cys Val Glu Trp Lys Gly Thr
350 355 360
Ser Gln Leu Ser Ala Trp His Met Val Lys Glu Thr Val Leu Gly
365 370 375
Ser Asp Arg Pro Gly Val Val Gly Ile Trp Leu Asn Leu Glu Glu
380 385 390
Gly Lys Leu Ala Phe Tyr Ser Val Asp Asn Gln Glu Lys Leu Leu
395 400 405
Tyr Glu Cys Thr Ile Ser Ala Ser Ser Pro Leu Tyr Pro Ala Phe
410 415 420
Trp Leu Tyr Gly Leu His Pro Gly Asn Tyr Leu Ile Ile Lys Gln
425 430 435
Val Lys Val

<210> 173
<211> 106
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:397228.1.orf1:2002JAN18

<400> 173
Arg Arg Arg Arg Ala Met Ala Ala Gln Leu Leu Glu Glu Lys Leu
1 5 10 15
Thr Cys Ala Ile Cys Leu Gly Leu Tyr Gln Asp Pro Val Thr Leu
20 25 30
Pro Cys Gly His Asn Phe Cys Gly Ala Cys Ile Arg Asp Trp Trp
35 40 45
Asp Arg Cys Gly Lys Ala Cys Pro Glu Cys Arg Glu Pro Phe Pro
50 55 60
Asp Gly Ala Glu Leu Arg Arg Asn Val Ala Leu Ser Gly Val Leu
65 70 75
Glu Val Val Arg Ala Gly Pro Ala Arg Asp Pro Gly Pro Asp Pro
80 85 90
Gly Pro Gly Pro Asp Pro Ala Ala Arg Cys Pro Arg His Gly Arg
95 100 105
Pro

<210> 174
<211> 357
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:401325.41.orf2:2002JAN18

<400> 174
Arg Trp Pro Pro Pro Asp Ala Gly Leu Cys Gly Ser Gly Pro Leu
1 5 10 15
Ser Ser Pro Ser Cys Cys Arg Tyr Arg Arg Cys Cys Arg Arg Leu
20 25 30
Arg Pro Pro Leu Arg Ser Val Val Gln Pro Gly Pro Arg Thr Met
35 40 45
Ser Leu Ser Arg Ser Glu Glu Met His Arg Leu Thr Glu Asn Val
50 55 60
Tyr Lys Thr Ile Met Glu Gln Phe Asn Pro Ser Leu Arg Asn Phe
65 70 75
Ile Ala Met Gly Lys Asn Tyr Glu Lys Ala Leu Ala Gly Val Thr
80 85 90
Tyr Ala Ala Lys Gly Tyr Phe Asp Ala Leu Val Lys Met Gly Glu
95 100 105
Leu Ala Ser Glu Ser Gln Gly Ser Lys Glu Leu Gly Asp Val Leu
110 115 120
Phe Gln Met Ala Glu Val His Arg Gln Ile Gln Asn Gln Leu Glu
125 130 135
Glu Met Leu Lys Ser Phe His Asn Glu Leu Leu Thr Gln Leu Glu
140 145 150
Gln Lys Val Glu Leu Asp Ser Arg Tyr Leu Ser Ala Ala Leu Lys
155 160 165
Lys Tyr Gln Thr Glu Gln Arg Ser Lys Gly Asp Ala Leu Asp Lys
170 175 180
Cys Gln Ala Glu Leu Lys Lys Leu Arg Lys Lys Ser Gln Gly Ser
185 190 195

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Lys Asn Pro Gln Lys Tyr Ser Asp Lys Glu Leu Gln Tyr Ile Asp
                200                 205                 210
Ala Ile Ser Asn Lys Gln Gly Glu Leu Glu Asn Tyr Val Ser Asp
                215                 220                 225
Gly Tyr Lys Thr Ala Leu Thr Glu Glu Arg Arg Arg Phe Cys Phe
                230                 235                 240
Leu Val Glu Lys Gln Cys Ala Val Ala Lys Asn Ser Ala Ala Tyr
                245                 250                 255
His Ser Lys Gly Lys Glu Leu Leu Ala Gln Lys Leu Pro Leu Trp
                260                 265                 270
Gln Gln Ala Cys Ala Asp Pro Ser Lys Ile Pro Glu Arg Ala Val
                275                 280                 285
Gln Leu Met Gln Gln Val Ala Ser Asn Gly Ala Thr Leu Pro Ser
                290                 295                 300
Ala Cys Arg Pro Pro Ser Gln Pro Gly His Phe Arg Pro His Ser
                305                 310                 315
Gly Gly Gln Ala Pro Ala Gly Ala Pro Arg Ala Gly Thr Val Arg
                320                 325                 330
Gly Ala Asp Val Cys Pro Gly Glu His Thr His His Glu Arg Arg
                335                 340                 345
His Arg Pro Gly Trp Arg Gly Leu Gln Pro Val Gly
                350                 355

<210> 175
<211> 266
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:402029.14.orf3:2002JAN18

<400> 175
Met Ala Leu Phe Ser Cys Arg Asn Ala Val Glu Glu Gly Lys Gly
 1               5                  10                  15
Ile Phe Tyr Asn Ile Lys Asn Phe Val Arg Phe Gln Leu Ser Thr
                20                  25                  30
Ser Ile Ser Ala Leu Ser Leu Ile Thr Leu Ser Thr Val Phe Asn
                35                  40                  45
Leu Pro Ser Pro Leu Asn Ala Met Gln Ile Leu Trp Ile Asn Ile
                50                  55                  60
Ile Met Asp Gly Pro Pro Ala Gln Arg Ser Ser Gln Lys Thr Glu
                65                  70                  75
Val Cys Cys Thr Gly Val Arg Leu Gly Val Glu Gly Arg Gly Glu
                80                  85                  90
Ser Thr Trp Ala Gly Arg Ala Gly Leu Gly Val Glu Pro Val Asp
                95                  100                 105
Lys Asp Ala Phe Arg Gln Pro Pro Arg Ser Val Arg Asp Thr Ile
                110                 115                 120
Leu Ser Arg Ala Leu Ile Leu Lys Ile Leu Met Ser Ala Ala Ile
                125                 130                 135
Ile Ile Ser Gly Thr Leu Phe Ile Phe Trp Lys Glu Met Pro Glu
                140                 145                 150
Asp Arg Ala Ser Thr Pro Arg Thr Thr Thr Met Thr Phe Thr Cys
                155                 160                 165
Phe Val Phe Phe Asp Leu Phe Asn Ala Leu Thr Cys Arg Ser Gln
                170                 175                 180
Thr Lys Leu Ile Phe Glu Ile Gly Phe Leu Arg Asn His Met Phe
                185                 190                 195
Leu Tyr Ser Val Leu Gly Ser Ile Leu Gly Gln Leu Ala Val Ile
                200                 205                 210
Tyr Ile Pro Pro Leu Gln Arg Val Phe Gln Thr Glu Asn Leu Gly
                215                 220                 225
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Ala Leu Asp Leu Leu Phe Leu Thr Gly Leu Ala Ser Ser Val Phe
230 235 240
Ile Leu Ser Glu Leu Leu Lys Leu Cys Glu Lys Tyr Cys Cys Ser
245 250 255
Pro Lys Arg Val Gln Met His Pro Glu Asp Val
260 265

<210> 176
<211> 470
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:407233.2.orf3:2002JAN18

<400> 176
Pro Arg Cys Pro Cys His Gln Asp Leu His Met Pro Ser Cys Val
1 5 10 15
Pro Pro Gly Val Pro Val Ser Asn Val Asn Leu Glu Ile Arg Pro
20 25 30
Thr Gly Gly Gln Leu Ile Glu Gly Glu Asn Met Val Leu Ile Cys
35 40 45
Ser Val Ala Gln Gly Ser Gly Thr Val Thr Phe Ser Trp His Lys
50 55 60
Glu Gly Arg Val Arg Ser Leu Gly Arg Lys Thr Gln Arg Ser Leu
65 70 75
Leu Ala Glu Leu His Val Leu Thr Val Lys Glu Ser Asp Ala Gly
80 85 90
Arg Tyr Tyr Cys Ala Ala Asp Asn Val His Ser Pro Ile Leu Ser
95 100 105
Thr Trp Ile Arg Val Thr Val Arg Ile Pro Val Ser His Pro Val
110 115 120
Leu Thr Phe Arg Ala Pro Arg Ala His Thr Val Val Gly Asp Leu
125 130 135
Leu Glu Leu His Cys Glu Ser Leu Arg Gly Ser Pro Pro Ile Leu
140 145 150
Tyr Arg Phe Tyr His Glu Asp Val Thr Leu Gly Asn Ser Ser Ala
155 160 165
Pro Ser Gly Gly Gly Ala Ser Phe Asn Leu Ser Leu Thr Ala Glu
170 175 180
His Ser Gly Asn Tyr Ser Cys Asp Ala Asp Asn Gly Leu Gly Ala
185 190 195
Gln His Ser His Gly Val Ser Leu Arg Val Thr Val Pro Val Ser
200 205 210
Arg Pro Val Leu Thr Leu Arg Ala Pro Gly Ala Gln Ala Val Val
215 220 225
Gly Asp Leu Leu Glu Leu His Cys Glu Ser Leu Arg Gly Ser Phe
230 235 240
Pro Ile Leu Tyr Trp Phe Tyr His Glu Asp Asp Thr Leu Gly Asn
245 250 255
Ile Ser Ala His Ser Gly Gly Gly Ala Ser Phe Asn Leu Ser Leu
260 265 270
Thr Thr Glu His Ser Gly Asn Tyr Ser Cys Glu Ala Asp Asn Gly
275 280 285
Leu Gly Ala Gln His Ser Lys Val Val Thr Leu Asn Val Thr Gly
290 295 300
Thr Ser Arg Asn Arg Thr Gly Leu Thr Ala Ala Gly Ile Thr Gly
305 310 315
Leu Val Leu Ser Ile Leu Val Leu Ala Ala Ala Ala Ala Leu Leu
320 325 330
His Tyr Ala Arg Ala Arg Arg Lys Pro Gly Gly Leu Ser Ala Thr
335 340 345

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Gly Thr Ser Ser His Ser Pro Ser Glu Cys Gln Glu Pro Ser Ser
                350                 355                 360
Ser Arg Pro Ser Arg Ile Asp Pro Gln Glu Pro Thr His Ser Lys
                365                 370                 375
Pro Leu Ala Pro Met Glu Leu Glu Pro Met Tyr Ser Asn Val Asn
                380                 385                 390
Pro Gly Asp Ser Asn Pro Ile Tyr Ser Gln Ile Trp Ser Ile Gln
                395                 400                 405
His Thr Lys Glu Asn Ser Ala Asn Cys Pro Met Met His Gln Glu
                410                 415                 420
His Glu Glu Leu Thr Val Leu Tyr Ser Glu Leu Lys Lys Thr His
                425                 430                 435
Pro Asp Asp Ser Ala Gly Glu Ala Ser Ser Arg Gly Arg Ala His
                440                 445                 450
Glu Glu Asp Asp Glu Glu Asn Tyr Glu Asn Val Pro Arg Val Leu
                455                 460                 465
Leu Ala Ser Asp His
                470

<210> 177
<211> 938
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:407346.1.orf3:2002JAN18

<400> 177
Arg Leu Glu Thr Ala Leu Lys Phe Leu Glu Gly Arg Lys Ser Met
  1               5                  10                  15
His Arg Gly Ser Pro Ile Lys Leu Val Asn Ile Asn Ser Thr Asp
                 20                  25                  30
Ile Ala Asp Gly Arg Pro Ser Ile Val Leu Gly Leu Met Trp Thr
                 35                  40                  45
Ile Ile Leu Tyr Phe Gln Ile Glu Glu Leu Thr Ser Asn Leu Pro
                 50                  55                  60
Gln Leu Gln Ser Leu Ser Ser Ser Ala Ser Ser Val Asp Ser Ile
                 65                  70                  75
Val Ser Ser Glu Thr Pro Ser Pro Pro Ser Lys Arg Lys Val Thr
                 80                  85                  90
Thr Lys Ile Gln Gly Asn Ala Lys Lys Ala Leu Leu Lys Trp Val
                 95                 100                 105
Gln Tyr Thr Ala Gly Lys Gln Thr Gly Ile Glu Val Lys Asp Phe
                110                 115                 120
Gly Lys Ser Trp Arg Ser Gly Val Ala Phe His Ser Val Ile His
                125                 130                 135
Ala Ile Arg Pro Glu Leu Val Asp Leu Glu Thr Val Lys Gly Arg
                140                 145                 150
Ser Asn Arg Glu Asn Leu Glu Asp Ala Phe Thr Ile Ala Glu Thr
                155                 160                 165
Glu Leu Gly Ile Pro Arg Leu Leu Asp Pro Glu Asp Val Asp Val
                170                 175                 180
Asp Lys Pro Asp Glu Lys Ser Ile Met Thr Tyr Val Ala Gln Phe
                185                 190                 195
Leu Lys His Tyr Pro Asp Ile His Asn Ala Ser Thr Asp Gly Gln
                200                 205                 210
Glu Asp Asp Glu Ile Leu Pro Gly Phe Pro Ser Phe Ala Asn Ser
                215                 220                 225
Val Gln Asn Phe Lys Arg Glu Asp Arg Val Ile Phe Lys Glu Met
                230                 235                 240
Lys Val Trp Ile Glu Gln Phe Glu Arg Asp Leu Thr Arg Ala Gln
                245                 250                 255
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Met Val Glu Ser Asn Leu Gln Asp Lys Tyr Gln Ser Phe Lys His
260 265 270
Phe Arg Val Gln Tyr Glu Met Lys Arg Lys Gln Ile Glu His Leu
275 280 285
Ile Gln Pro Leu His Arg Asp Gly Lys Leu Ser Leu Asp Gln Ala
290 295 300
Leu Val Lys Gln Ser Trp Asp Arg Val Thr Ser Arg Leu Phe Asp
305 310 315
Trp His Ile Gln Leu Asp Lys Ser Leu Pro Ala Pro Leu Gly Thr
320 325 330
Ile Gly Ala Trp Leu Tyr Arg Ala Glu Val Ala Leu Arg Glu Glu
335 340 345
Ile Thr Val Gln Gln Val His Glu Glu Thr Ala Asn Thr Ile Gln
350 355 360
Arg Lys Leu Glu Gln His Lys Asp Leu Leu Gln Asn Thr Asp Ala
365 370 375
His Lys Arg Ala Phe His Glu Ile Tyr Arg Thr Arg Ser Val Asn
380 385 390
Gly Ile Pro Val Pro Pro Asp Gln Leu Glu Asp Met Ala Glu Arg
395 400 405
Phe His Phe Val Ser Ser Thr Ser Glu Leu His Leu Met Lys Met
410 415 420
Glu Phe Leu Glu Leu Lys Tyr Arg Leu Leu Ser Leu Leu Val Leu
425 430 435
Ala Glu Ser Lys Leu Lys Ser Trp Ile Ile Lys Tyr Gly Arg Arg
440 445 450
Glu Ser Val Glu Gln Leu Leu Gln Asn Tyr Val Ser Phe Ile Glu
455 460 465
Asn Ser Lys Phe Phe Glu Gln Tyr Glu Val Thr Tyr Gln Ile Leu
470 475 480
Lys Gln Thr Ala Glu Met Tyr Val Lys Ala Asp Gly Ser Val Glu
485 490 495
Glu Ala Glu Asn Val Met Lys Phe Met Asn Glu Thr Thr Ala Gln
500 505 510
Trp Arg Asn Leu Ser Val Glu Val Arg Ser Val Arg Ser Met Leu
515 520 525
Glu Glu Val Ile Ser Asn Trp Asp Arg Tyr Gly Asn Thr Val Ala
530 535 540
Ser Leu Gln Ala Trp Leu Glu Asp Ala Glu Lys Met Leu Asn Gln
545 550 555
Ser Glu Asn Ala Lys Lys Asp Phe Phe Arg Asn Leu Pro His Trp
560 565 570
Ile Gln Gln His Thr Ala Met Asn Asp Ala Gly Asn Phe Leu Ile
575 580 585
Glu Thr Cys Asp Glu Met Val Ser Arg Asp Leu Lys Gln Gln Leu
590 595 600
Leu Leu Leu Asn Gly Arg Trp Arg Glu Leu Phe Met Glu Val Lys
605 610 615
Gln Tyr Ala Gln Ala Asp Glu Met Asp Arg Met Lys Lys Glu Tyr
620 625 630
Thr Asp Cys Val Val Thr Leu Ser Ala Phe Ala Thr Glu Ala His
635 640 645
Lys Lys Leu Ser Glu Pro Leu Glu Val Ser Phe Met Asn Val Lys
650 655 660
Leu Leu Ile Gln Asp Leu Glu Asp Ile Glu Gln Arg Val Pro Val
665 670 675
Met Asp Ala Gln Tyr Lys Ile Ile Thr Lys Thr Ala His Leu Ile
680 685 690
Thr Lys Glu Ser Pro Gln Glu Glu Gly Lys Glu Met Phe Ala Thr
695 700 705
Met Ser Lys Leu Lys Glu Gln Leu Thr Lys Val Lys Glu Cys Tyr
710 715 720
Ser Pro Leu Leu Tyr Glu Ser Gln Gln Leu Leu Ile Pro Leu Glu

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                725                     730                     735
Glu Leu Glu Lys Gln Met Thr Ser Phe Tyr Asp Ser Leu Gly Lys
                740                     745                     750
Ile Asn Glu Ile Ile Thr Val Leu Glu Arg Glu Ala Gln Ser Ser
                755                     760                     765
Ala Leu Phe Lys Gln Lys His Gln Glu Leu Leu Ala Cys Gln Glu
                770                     775                     780
Asn Cys Lys Lys Thr Leu Thr Leu Ile Glu Lys Gly Ser Gln Ser
                785                     790                     795
Val Gln Lys Phe Val Thr Leu Ser Asn Val Leu Lys His Phe Asp
                800                     805                     810
Gln Thr Arg Leu Gln Arg Gln Ile Ala Asp Ile His Val Ala Phe
                815                     820                     825
Gln Ser Met Val Lys Lys Thr Gly Asp Trp Lys Lys His Val Glu
                830                     835                     840
Thr Asn Ser Arg Leu Met Lys Lys Phe Glu Glu Ser Arg Ala Glu
                845                     850                     855
Leu Glu Lys Val Leu Arg Ile Ala Gln Glu Gly Leu Glu Glu Lys
                860                     865                     870
Gly Asp Pro Glu Glu Leu Leu Arg Arg His Thr Glu Phe Phe Ser
                875                     880                     885
Gln Leu Asp Gln Arg Val Leu Asn Ala Phe Leu Lys Ala Cys Asp
                890                     895                     900
Glu Leu Thr Asp Ile Phe Gln Ser Arg Ser Ser Arg Gly Cys Arg
                905                     910                     915
Lys Leu Phe Glu Ser Ser Thr Asn Asn Gly Arg Ile Phe Lys Glu
                920                     925                     930
Lys Pro Leu Ile Ile Cys Phe Ile
                935

<210> 178
<211> 928
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:407689.7.orf3:2002JAN18

<400> 178
Ser Gly Tyr Gly Arg Lys Cys Leu Glu Val Leu Asn Leu Gly Val
  1               5                      10                      15
Leu Asn Arg Met Asn His Ile Lys His Val Asp Leu Arg Met Asn
                 20                      25                      30
His Leu Lys Thr Met Val Ile Glu Asn Leu Glu Gly Asn Lys His
                 35                      40                      45
Ile Thr His Val Asp Leu Arg Asp Asn Arg Leu Thr Asp Leu Asp
                 50                      55                      60
Leu Ser Ser Leu Cys Ser Leu Glu Gln Leu His Cys Gly Arg Asn
                 65                      70                      75
Gln Leu Arg Glu Leu Thr Leu Ser Gly Phe Ser Leu Arg Thr Leu
                 80                      85                      90
Tyr Ala Ser Ser Asn Arg Leu Thr Ala Val Asn Val Tyr Pro Val
                 95                     100                     105
Pro Ser Leu Leu Thr Phe Leu Asp Leu Ser Arg Asn Leu Leu Glu
                110                     115                     120
Cys Val Pro Asp Trp Ala Cys Glu Ala Lys Lys Ile Glu Val Leu
                125                     130                     135
Asp Val Ser Tyr Asn Leu Leu Thr Glu Val Pro Val Arg Ile Leu
                140                     145                     150
Ser Ser Leu Ser Leu Arg Lys Leu Met Leu Gly His Asn His Val
                155                     160                     165
Gln Asn Leu Pro Thr Leu Val Glu His Ile Pro Leu Glu Val Leu
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170 175 180
Asp Leu Gln His Asn Ala Leu Thr Arg Leu Pro Asp Thr Leu Phe
185 190 195
Ser Lys Ala Leu Asn Leu Arg Tyr Leu Asn Ala Ser Ala Asn Ser
200 205 210
Leu Glu Ser Leu Pro Ser Ala Cys Thr Gly Glu Glu Ser Leu Ser
215 220 225
Met Leu Gln Leu Leu Tyr Leu Thr Asn Asn Leu Leu Thr Asp Gln
230 235 240
Cys Ile Pro Val Leu Val Gly His Leu His Leu Arg Ile Leu His
245 250 255
Leu Ala Asn Asn Gln Leu Gln Thr Phe Pro Ala Ser Lys Leu Asn
260 265 270
Lys Leu Glu Gln Leu Glu Glu Leu Asn Leu Ser Gly Asn Lys Leu
275 280 285
Lys Thr Ile Pro Thr Thr Ile Ala Asn Cys Lys Arg Leu His Thr
290 295 300
Leu Val Ala His Ser Asn Asn Ile Ser Ile Phe Pro Glu Ile Leu
305 310 315
Gln Leu Pro Gln Ile Gln Phe Val Asp Leu Ser Cys Asn Asp Leu
320 325 330
Thr Glu Ile Leu Ile Pro Glu Ala Leu Pro Ala Thr Leu Gln Asp
335 340 345
Leu Asp Leu Thr Gly Asn Thr Asn Leu Val Leu Glu His Lys Thr
350 355 360
Leu Asp Ile Phe Ser His Ile Thr Thr Leu Lys Ile Asp Gln Lys
365 370 375
Pro Leu Pro Thr Thr Asp Ser Thr Val Thr Ser Thr Phe Trp Ser
380 385 390
His Gly Leu Ala Glu Met Ala Gly Gln Arg Asn Lys Leu Cys Val
395 400 405
Ser Ala Leu Ala Met Asp Ser Phe Ala Glu Gly Val Gly Ala Val
410 415 420
Tyr Gly Met Phe Asp Gly Asp Arg Asn Glu Glu Leu Pro Arg Leu
425 430 435
Leu Gln Cys Thr Met Ala Asp Val Leu Leu Glu Glu Val Gln Gln
440 445 450
Ser Thr Asn Asp Thr Val Phe Met Ala Asn Thr Phe Leu Val Ser
455 460 465
His Arg Lys Leu Gly Met Ala Gly Gln Lys Leu Gly Ser Ser Ala
470 475 480
Leu Leu Cys Tyr Ile Arg Pro Asp Thr Ala Asp Pro Ala Ser Ser
485 490 495
Phe Ser Leu Thr Val Ala Asn Val Gly Thr Cys Gln Ala Val Leu
500 505 510
Cys Arg Gly Gly Lys Pro Val Pro Leu Ser Lys Val Phe Ser Leu
515 520 525
Glu Gln Asp Pro Glu Glu Ala Gln Arg Val Lys Asp Gln Lys Ala
530 535 540
Ile Ile Thr Glu Asp Asn Lys Val Asn Gly Val Thr Cys Cys Thr
545 550 555
Arg Met Leu Gly Cys Thr Tyr Leu Tyr Pro Trp Ile Leu Pro Lys
560 565 570
Pro His Ile Ser Ser Thr Pro Leu Thr Ile Gln Asp Glu Leu Leu
575 580 585
Ile Leu Gly Asn Lys Ala Leu Trp Glu His Leu Ser Tyr Thr Glu
590 595 600
Ala Val Asn Ala Val Arg His Val Gln Asp Pro Leu Ala Ala Ala
605 610 615
Lys Lys Leu Cys Thr Leu Ala Gln Ser Tyr Gly Cys Gln Asp Asn
620 625 630
Val Gly Ala Met Val Val Tyr Leu Asn Ile Gly Glu Glu Gly Cys
635 640 645

Thr Cys Glu Met Asn Gly Leu Thr Leu Pro Gly Pro Val Gly Phe
650 655 660
Ala Ser Thr Thr Thr Ile Lys Asp Ala Pro Lys Pro Ala Thr Pro
665 670 675
Ser Ser Ser Ser Gly Ile Ala Ser Glu Phe Ser Ser Glu Met Ser
680 685 690
Thr Ser Glu Val Ser Ser Glu Val Gly Ser Thr Ala Ser Asp Glu
695 700 705
His Asn Ala Gly Gly Leu Asp Thr Ala Leu Leu Pro Arg Pro Glu
710 715 720
Arg Arg Cys Ser Leu His Pro Thr Pro Thr Ser Gly Leu Phe Gln
725 730 735
Arg Gln Pro Ser Ser Ala Thr Phe Ser Ser Asn Gln Ser Asp Asn
740 745 750
Gly Leu Asp Ser Asp Asp Asp Gln Pro Val Glu Gly Val Ile Thr
755 760 765
Asn Gly Ser Lys Val Glu Val Glu Val Asp Ile His Cys Cys Arg
770 775 780
Gly Arg Asp Leu Glu Asn Ser Pro Pro Leu Ile Glu Ser Ser Pro
785 790 795
Thr Leu Cys Ser Glu Glu His Ala Arg Gly Ser Cys Phe Gly Ile
800 805 810
Arg Arg Gln Asn Ser Val Asn Ser Gly Met Leu Leu Pro Met Ser
815 820 825
Lys Asp Arg Met Glu Leu Gln Lys Ser Pro Ser Thr Ser Cys Leu
830 835 840
Tyr Gly Lys Lys Leu Ser Asn Gly Ser Ile Val Pro Leu Glu Asp
845 850 855
Ser Leu Asn Leu Ile Glu Val Ala Thr Glu Val Pro Lys Arg Lys
860 865 870
Thr Gly Tyr Phe Ala Ala Pro Thr Gln Met Glu Pro Glu Asp Gln
875 880 885
Phe Val Val Pro His Asp Leu Glu Glu Glu Val Lys Glu Gln Met
890 895 900
Lys Gln His Gln Asp Ser Arg Leu Glu Pro Glu Pro His Glu Glu
905 910 915
Asp Arg Thr Glu Pro Pro Glu Glu Phe Asp Thr Ala Leu
920 925

<210> 179
<211> 304
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:407700.1.orf2:2002JAN18

<400> 179
Pro Gly Pro Trp Ala Pro Ala Arg Ala Gly Ala Gly Ala Ser Gly
1 5 10 15
Met Ala Phe Arg Gln Ala Leu Gln Leu Ala Ala Cys Gly Leu Ala
20 25 30
Gly Gly Ser Ala Ala Val Leu Phe Ser Ala Val Ala Val Gly Lys
35 40 45
Pro Arg Ala Gly Gly Asp Ala Glu Pro Arg Pro Ala Glu Pro Pro
50 55 60
Ala Trp Ala Gly Gly Ala Arg Pro Gly Pro Gly Val Trp Asp Pro
65 70 75
Asn Trp Asp Arg Arg Glu Pro Leu Ser Leu Ile Asn Val Arg Lys
80 85 90
Arg Asn Val Glu Ser Gly Glu Glu Glu Leu Ala Ser Lys Leu Asp
95 100 105

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His Tyr Lys Ala Lys Ala Thr Arg His Ile Phe Leu Ile Arg His
                110                 115                 120
Ser Gln Tyr His Val Asp Gly Ser Leu Glu Lys Asp Arg Thr Leu
                125                 130                 135
Thr Pro Leu Gly Arg Glu Gln Ala Glu Leu Thr Gly Leu Arg Leu
                140                 145                 150
Ala Ser Leu Gly Leu Lys Phe Asn Lys Ile Val His Ser Ser Met
                155                 160                 165
Thr Arg Ala Ile Glu Thr Thr Asp Ile Ile Ser Arg His Leu Pro
                170                 175                 180
Gly Val Cys Lys Val Ser Thr Asp Leu Leu Arg Glu Gly Ala Pro
                185                 190                 195
Ile Glu Pro Asp Pro Pro Val Ser His Trp Lys Pro Glu Ala Val
                200                 205                 210
Gln Tyr Tyr Glu Asp Gly Ala Arg Ile Glu Ala Ala Phe Arg Asn
                215                 220                 225
Tyr Ile His Arg Ala Asp Ala Arg Gln Glu Glu Asp Ser Tyr Glu
                230                 235                 240
Ile Phe Ile Cys His Ala Asn Val Ile Arg Tyr Ile Val Cys Arg
                245                 250                 255
Ala Leu Gln Phe Pro Pro Glu Gly Trp Leu Arg Leu Ser Leu Asn
                260                 265                 270
Asn Gly Ser Ile Thr His Leu Val Ile Arg Pro Asn Gly Arg Val
                275                 280                 285
Ala Leu Arg Thr Leu Gly Asp Thr Gly Phe Met Pro Pro Asp Lys
                290                 295                 300
Ile Thr Arg Ser


<210> 180
<211> 320
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:410461.92.orf3:2002JAN18

<400> 180
Ala Pro Ala Pro Glu Pro Gly Pro Arg Ala Ala Ala Ala Ala Gly
  1               5                  10                  15
Gly Thr Met Ser Cys Ala Gly Arg Ala Gly Pro Ala Arg Leu Ala
                 20                  25                  30
Ala Leu Ala Leu Leu Thr Cys Ser Leu Trp Pro Ala Arg Ala Asp
                 35                  40                  45
Asn Ala Ser Gln Glu Tyr Tyr Thr Ala Leu Ile Asn Val Thr Val
                 50                  55                  60
Gln Glu Pro Gly Arg Gly Ala Pro Leu Thr Phe Arg Ile Asp Arg
                 65                  70                  75
Gly Arg Tyr Gly Leu Asp Ser Pro Lys Ala Glu Val Arg Gly Gln
                 80                  85                  90
Val Leu Ala Pro Leu Pro Leu His Gly Val Ala Asp His Leu Gly
                 95                 100                 105
Cys Asp Pro Gln Thr Arg Phe Phe Val Pro Pro Asn Ile Lys Gln
                110                 115                 120
Trp Ile Ala Leu Leu Gln Arg Gly Asn Cys Thr Phe Lys Glu Lys
                125                 130                 135
Ile Ser Arg Ala Ala Phe His Asn Ala Val Ala Val Val Ile Tyr
                140                 145                 150
Asn Asn Lys Ser Lys Glu Glu Pro Val Thr Met Thr His Pro Gly
                155                 160                 165
Thr Gly Asp Ile Ile Ala Val Met Ile Thr Glu Leu Arg Gly Lys
                170                 175                 180
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Asp Ile Leu Ser Tyr Leu Glu Asn Phe Ser Arg Gly Ser Leu Val
                185                 190                 195
Phe Val Ser Ile Ser Phe Ile Val Leu Met Ile Ile Ser Ser Ala
                200                 205                 210
Trp Leu Ile Phe Tyr Phe Ile Gln Lys Ile Arg Tyr Thr Asn Ala
                215                 220                 225
Arg Asp Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala Lys Lys Ala
                230                 235                 240
Ile Ser Lys Leu Thr Thr Arg Thr Val Lys Lys Gly Asp Lys Glu
                245                 250                 255
Thr Asp Pro Asp Phe Asp His Cys Ala Val Cys Ile Glu Ser Tyr
                260                 265                 270
Lys Gln Asn Asp Val Val Arg Ile Leu Pro Cys Lys His Val Phe
                275                 280                 285
His Lys Ser Cys Val Asp Pro Trp Leu Ser Glu His Cys Thr Cys
                290                 295                 300
Pro Met Cys Lys Leu Asn Ile Leu Lys Ala Leu Gly Asn Cys Ala
                305                 310                 315
Glu Phe Ala Met Tyr
                320

&lt;210&gt; 181
&lt;211&gt; 358
&lt;212&gt; PRT
&lt;213&gt; Homo sapiens

&lt;220&gt;
&lt;221&gt; misc_feature
&lt;223&gt; Incyte ID No: LG:411043.3.orf2:2002JAN18

&lt;400&gt; 181
Asn His Cys Pro Thr Arg Ala Met Ile Val Gln Arg Val Val Leu
  1             5                   10                  15
Asn Ser Arg Pro Gly Lys Asn Gly Asn Pro Val Ala Glu Asn Phe
                20                  25                  30
Arg Met Glu Glu Val Tyr Leu Pro Asp Asn Ile Asn Glu Gly Gln
                35                  40                  45
Val Gln Val Arg Thr Leu Tyr Leu Ser Val Asp Pro Tyr Met Arg
                50                  55                  60
Cys Arg Met Asn Glu Asp Thr Gly Thr Asp Tyr Ile Thr Pro Trp
                65                  70                  75
Gln Leu Ser Gln Val Val Asp Gly Gly Gly Ile Gly Ile Ile Glu
                80                  85                  90
Glu Ser Lys His Thr Asn Leu Thr Lys Gly Asp Phe Val Thr Ser
                95                  100                 105
Phe Tyr Trp Pro Trp Gln Thr Lys Val Ile Leu Asp Gly Asn Ser
                110                 115                 120
Leu Glu Lys Val Asp Pro Gln Leu Val Asp Gly His Leu Ser Tyr
                125                 130                 135
Phe Leu Gly Ala Ile Gly Met Pro Gly Leu Thr Ser Leu Ile Gly
                140                 145                 150
Ile Gln Glu Lys Gly His Ile Thr Ala Gly Ser Asn Lys Thr Met
                155                 160                 165
Val Val Ser Gly Ala Ala Gly Ala Cys Gly Ser Val Ala Gly Gln
                170                 175                 180
Ile Gly His Phe Leu Gly Cys Ser Arg Val Val Gly Ile Cys Gly
                185                 190                 195
Thr His Glu Lys Cys Ile Leu Leu Thr Ser Glu Leu Gly Phe Asp
                200                 205                 210
Ala Ala Ile Asn Tyr Lys Lys Asp Asn Val Ala Glu Gln Leu Arg
                215                 220                 225
Glu Ser Cys Pro Ala Gly Val Asp Val Tyr Phe Asp Asn Val Gly
                230                 235                 240
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Gly Asn Ile Ser Asp Thr Val Ile Ser Gln Met Asn Glu Asn Ser
                245                 250                 255
His Ile Ile Leu Cys Gly Gln Ile Ser Gln Tyr Asn Lys Asp Val
                260                 265                 270
Pro Tyr Pro Pro Pro Leu Ser Pro Ala Ile Glu Ala Ile Gln Lys
                275                 280                 285
Glu Arg Asn Ile Thr Arg Glu Arg Phe Leu Val Leu Asn Tyr Lys
                290                 295                 300
Asp Lys Phe Glu Pro Gly Ile Leu Gln Leu Ser Gln Trp Phe Lys
                305                 310                 315
Glu Gly Lys Leu Lys Ile Lys Glu Thr Val Ile Asn Gly Leu Glu
                320                 325                 330
Asn Met Gly Ala Ala Phe Gln Ser Met Met Thr Gly Gly Asn Ile
                335                 340                 345
Gly Lys Gln Ile Val Cys Ile Ser Glu Glu Ile Ser Leu
                350                 355

<210> 182
<211> 438
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:438690.47.orf1:2002JAN18

<400> 182
Arg Val Arg Ala Gly Leu Pro Cys Pro Met Cys Ser Gly Arg Phe
  1             5                   10                  15
Gln Asn Ile Gln Val Asn Pro Asp Phe Pro Arg Gly Arg Ile Ser
                20                  25                  30
Asn Ser Phe Arg Arg Thr Ser Ser Thr Glu Asn Lys Thr Lys Thr
                35                  40                  45
Leu Gly Lys Leu His Gln Glu Pro Arg Gln Leu Gln Ser Asp Gly
                50                  55                  60
Lys Arg Lys Ile Leu Leu Glu Glu Leu Ala Asn Ser Asp Pro Lys
                65                  70                  75
Leu Ala Leu Thr Gly Val Pro Ile Val Gln Trp Pro Lys Arg Asp
                80                  85                  90
Lys Leu Lys Phe Pro Thr Arg Pro Lys Val Arg Val Pro Thr Ile
                95                  100                 105
Pro Ile Thr Lys Pro His Thr Met Lys Pro Ala Pro Arg Leu Thr
                110                 115                 120
Pro Val Arg Pro Ala Ala Ala Ser Pro Ile Val Ser Gly Ala Arg
                125                 130                 135
Arg Arg Arg Val Arg Cys Arg Lys Cys Lys Ala Cys Val Gln Gly
                140                 145                 150
Glu Cys Gly Val Cys His Tyr Cys Arg Asp Met Lys Lys Phe Gly
                155                 160                 165
Gly Pro Gly Arg Met Lys Gln Ser Cys Val Leu Arg Gln Cys Leu
                170                 175                 180
Ala Pro Arg Leu Pro His Ser Val Thr Cys Ser Leu Cys Gly Glu
                185                 190                 195
Val Asp Gln Asn Glu Glu Thr Gln Asp Phe Glu Lys Lys Leu Met
                200                 205                 210
Glu Cys Cys Ile Cys Asn Glu Ile Val His Pro Gly Cys Leu Gln
                215                 220                 225
Met Asp Gly Glu Gly Leu Leu Asn Glu Glu Leu Pro Asn Cys Trp
                230                 235                 240
Glu Cys Pro Lys Cys Tyr Gln Glu Asp Ser Ser Glu Lys Ala Gln
                245                 250                 255
Lys Arg Lys Met Glu Glu Ser Asp Glu Glu Ala Val Gln Ala Lys
                260                 265                 270
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Val Leu Arg Pro Leu Arg Ser Cys Asp Glu Pro Leu Thr Pro Pro
                275                 280                 285
Pro His Ser Pro Thr Ser Met Leu Gln Leu Ile His Asp Pro Val
                290                 295                 300
Ser Pro Arg Gly Met Val Thr Arg Ser Ser Pro Gly Ala Gly Pro
                305                 310                 315
Ser Asp His His Ser Ala Ser Arg Asp Glu Arg Phe Lys Arg Arg
                320                 325                 330
Gln Leu Leu Arg Leu Gln Ala Thr Glu Arg Thr Met Val Arg Glu
                335                 340                 345
Lys Glu Asn Asn Pro Ser Gly Lys Lys Glu Leu Ser Glu Val Glu
                350                 355                 360
Lys Ala Lys Ile Arg Gly Ser Tyr Leu Thr Val Thr Leu Gln Arg
                365                 370                 375
Pro Thr Lys Glu Leu His Gly Thr Ser Ile Val Pro Lys Leu Gln
                380                 385                 390
Ala Ile Thr Ala Ser Ser Ala Asn Leu Arg His Ser Pro Arg Val
                395                 400                 405
Leu Val Gln His Cys Pro Ala Arg Thr Pro Gln Arg Gly Asp Glu
                410                 415                 420
Glu Gly Leu Gly Gly Ser Arg Arg Arg Lys Arg Arg Arg Arg Asp
                425                 430                 435
Gly Gly Arg


<210> 183
<211> 246
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:444677.81.orf1:2002JAN18

<400> 183
Gln Ala Leu Met Leu Val Ser Gly Arg Arg Arg Leu Leu Thr Ala
  1               5                  10                  15
Leu Leu Gln Ala Gln Lys Trp Pro Phe Gln Pro Ser Arg Asp Met
                 20                  25                  30
Arg Leu Val Gln Phe Arg Ala Pro His Leu Val Gly Pro His Leu
                 35                  40                  45
Gly Leu Glu Thr Gly Asn Gly Gly Gly Val Ile Asn Leu Asn Ala
                 50                  55                  60
Phe Asp Pro Thr Leu Pro Lys Thr Met Thr Gln Phe Leu Glu Gln
                 65                  70                  75
Gly Glu Ala Thr Leu Ser Val Ala Arg Arg Ala Leu Ala Ala Gln
                 80                  85                  90
Leu Pro Val Leu Pro Trp Ser Glu Val Thr Phe Leu Ala Pro Val
                 95                 100                 105
Thr Trp Pro Asp Lys Val Val Cys Val Gly Met Asn Tyr Val Asp
                110                 115                 120
His Cys Lys Glu Gln Asn Val Pro Val Pro Lys Glu Pro Ile Ile
                125                 130                 135
Phe Ser Lys Phe Ala Ser Ser Ile Val Gly Pro Tyr Asp Glu Val
                140                 145                 150
Val Leu Pro Pro Gln Ser Gln Glu Val Asp Trp Glu Val Glu Leu
                155                 160                 165
Ala Val Val Ile Gly Lys Lys Gly Lys His Ile Lys Ala Thr Asp
                170                 175                 180
Ala Met Ala His Val Ala Gly Phe Thr Val Ala His Asp Val Ser
                185                 190                 195
Ala Arg Asp Trp Leu Thr Arg Arg Asn Gly Lys Gln Trp Leu Leu
                200                 205                 210
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Gly Lys Thr Phe Asp Thr Phe Cys Pro Leu Gly Pro Ala Leu Val
                215                 220                 225
Thr Lys Asp Ser Val Ala Gly Arg Ser Leu Val Pro Ala Pro Trp
                230                 235                 240
Tyr Leu Pro Leu His Arg
                245

<210> 184
<211> 266
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:457464.24.orf3:2002JAN18

<400> 184
Gln Phe Ser Glu Gln Gln Pro Ser Tyr Gly Gly Gln Gln Gln Ser
 1              5                   10                  15
Tyr Gly Gln Gln Gln Ser Tyr Asn Pro Pro Gln Gly Tyr Gly Gln
                20                  25                  30
Gln Asn Gln Tyr Asn Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly
                35                  40                  45
Gly Gly Gly Asn Tyr Gly Gln Asp Gln Ser Ser Met Ser Ser Gly
                50                  55                  60
Gly Gly Ser Gly Gly Gly Tyr Gly Asn Gln Asp Gln Ser Gly Gly
                65                  70                  75
Gly Gly Ser Gly Gly Tyr Gly Gln Gln Asp Arg Gly Gly Arg Gly
                80                  85                  90
Arg Gly Gly Ser Gly Gly Ala Ala Ala Ala Ala Val Val Val Thr
                95                  100                 105
Thr Ala Ala Val Val Ala Met Asn Pro Glu Val Val Glu Val Ala
                110                 115                 120
Val Glu Ala Glu Val Ala Trp Gly Pro Arg Asp Gln Gly Ser Arg
                125                 130                 135
His Asp Ser Glu Gln Asp Asn Ser Asp Asn Asn Thr Ile Phe Val
                140                 145                 150
Gln Gly Leu Gly Glu Asn Val Thr Ile Glu Ser Val Ala Asp Tyr
                155                 160                 165
Phe Lys Gln Ile Gly Ile Ile Lys Thr Asn Lys Lys Thr Gly Gln
                170                 175                 180
Pro Met Ile Asn Leu Tyr Thr Asp Arg Glu Thr Gly Lys Leu Lys
                185                 190                 195
Gly Glu Ala Thr Val Ser Phe Asp Asp Pro Pro Ser Ala Lys Ala
                200                 205                 210
Ala Ile Asp Trp Phe Asp Gly Lys Glu Phe Ser Gly Asn Pro Ile
                215                 220                 225
Lys Val Ser Phe Ala Thr Arg Arg Ala Asp Phe Asn Arg Gly Gly
                230                 235                 240
Gly Asn Gly Arg Gly Gly Arg Gly Arg Gly Gly Pro Met Gly Arg
                245                 250                 255
Gly Gly Tyr Gly Gly Gly Gly Ser Ala Gly Trp
                260                 265

<210> 185
<211> 539
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:7684793.15.orf3:2002JAN18
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<400> 185

Lys Leu Gly Ser Met Glu Pro Ala Pro Ala Arg Ser Pro Arg Pro
1 5 10 15
Gln Gln Asp Pro Ala Arg Pro Gln Glu Pro Thr Met Pro Pro Pro
20 25 30
Glu Thr Pro Ser Glu Gly Arg Gln Pro Ser Pro Ser Pro Ser Pro
35 40 45
Thr Glu Arg Ala Pro Ala Ser Glu Glu Glu Phe Gln Phe Leu Arg
50 55 60
Cys Gln Gln Cys Gln Ala Glu Ala Lys Cys Pro Lys Leu Leu Pro
65 70 75
Cys Leu His Thr Leu Cys Ser Gly Cys Leu Glu Ala Ser Gly Met
80 85 90
Gln Cys Pro Ile Cys Gln Ala Pro Trp Pro Leu Gly Ala Asp Thr
95 100 105
Pro Ala Leu Asp Asn Val Phe Phe Glu Ser Leu Gln Arg Arg Leu
110 115 120
Ser Val Tyr Arg Gln Ile Val Asp Ala Gln Ala Val Cys Thr Arg
125 130 135
Cys Lys Glu Ser Ala Asp Phe Trp Cys Phe Glu Cys Glu Gln Leu
140 145 150
Leu Cys Ala Lys Cys Phe Glu Ala His Gln Trp Phe Leu Lys His
155 160 165
Glu Ala Arg Pro Leu Ala Glu Leu Arg Asn Gln Ser Val Arg Glu
170 175 180
Phe Leu Asp Gly Thr Arg Lys Thr Asn Asn Ile Phe Cys Ser Asn
185 190 195
Pro Asn His Arg Thr Pro Thr Leu Thr Ser Ile Tyr Cys Arg Gly
200 205 210
Cys Ser Lys Pro Leu Cys Cys Ser Cys Ala Leu Leu Asp Ser Ser
215 220 225
His Ser Glu Leu Lys Cys Asp Ile Ser Ala Glu Ile Gln Gln Arg
230 235 240
Gln Glu Glu Leu Asp Ala Met Thr Gln Ala Leu Gln Glu Gln Asp
245 250 255
Ser Ala Phe Gly Ala Val His Ala Gln Met His Ala Ala Val Gly
260 265 270
Gln Leu Gly Arg Ala Arg Ala Glu Thr Glu Glu Leu Ile Arg Glu
275 280 285
Arg Val Arg Gln Val Val Ala His Val Arg Ala Gln Glu Arg Glu
290 295 300
Leu Leu Glu Ala Val Asp Ala Arg Tyr Gln Arg Asp Tyr Glu Glu
305 310 315
Met Ala Ser Arg Leu Gly Arg Leu Asp Ala Val Leu Gln Arg Ile
320 325 330
Arg Thr Gly Ser Ala Leu Val Gln Arg Met Lys Cys Tyr Ala Ser
335 340 345
Asp Gln Glu Val Leu Asp Met His Gly Phe Leu Arg Gln Ala Leu
350 355 360
Cys Arg Leu Arg Gln Glu Glu Pro Gln Ser Leu Gln Ala Ala Val
365 370 375
Arg Thr Asp Gly Phe Asp Glu Phe Lys Val Arg Leu Gln Asp Leu
380 385 390
Ser Ser Cys Ile Thr Gln Gly Lys Asp Ala Ala Val Ser Lys Lys
395 400 405
Ala Ser Pro Glu Ala Ala Ser Thr Pro Arg Asp Pro Ile Asp Val
410 415 420
Asp Leu Ala Glu Glu Ala Glu Arg Val Lys Ala Gln Val Gln Ala
425 430 435
Leu Gly Leu Ala Glu Ala Gln Pro Met Ala Val Val Gln Ser Val
440 445 450
Pro Gly Ala His Pro Val Pro Val Tyr Ala Phe Ser Ile Lys Gly
455 460 465

Pro Ser Tyr Gly Glu Asp Val Ser Asn Thr Thr Thr Ala Gln Lys
470 475 480
Arg Lys Cys Ser Gln Thr Gln Cys Pro Arg Lys Val Ile Lys Met
485 490 495
Glu Ser Glu Glu Gly Lys Glu Ala Arg Leu Ala Arg Ser Ser Pro
500 505 510
Glu Gln Pro Arg Pro Ser Thr Ser Lys Ala Val Ser Pro Pro His
515 520 525
Leu Asp Gly Pro Pro Ser Pro Arg Ser Pro Val Ile Gly Ser
530 535

<210> 186
<211> 242
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:7687485.1.orf1:2002JAN18

<400> 186
Thr Gln Leu Thr Thr Asn Gln Thr Asn Pro Ser Gly Gln Ile Ser
1 5 10 15
Tyr Glu Cys Gly Gln Cys Gly Arg Tyr Phe Ile Gln Met Ala Asp
20 25 30
Phe His Arg His Glu Lys Cys His Thr Gly Glu Lys Ser Phe Glu
35 40 45
Cys Lys Glu Cys Gly Lys Tyr Phe Arg Tyr Asn Ser Leu Leu Ile
50 55 60
Arg His Gln Ile Ile His Thr Gly Lys Lys Pro Phe Lys Cys Lys
65 70 75
Glu Cys Gly Lys Gly Leu Ser Ser Asp Thr Ala Leu Ile Gln His
80 85 90
Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys
95 100 105
Gly Lys Ala Phe Ser Ser Ser Ser Val Phe Leu Gln His Gln Arg
110 115 120
Phe His Thr Gly Glu Lys Leu Tyr Glu Cys Asn Glu Cys Trp Lys
125 130 135
Thr Phe Ser Cys Ser Ser Ser Phe Thr Val His Gln Arg Met His
140 145 150
Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys Arg Leu
155 160 165
Ser Ser Asn Thr Ala Leu Thr Gln His Gln Arg Ile His Thr Gly
170 175 180
Glu Lys Pro Phe Glu Cys Lys Glu Cys Gly Lys Ala Phe Asn Gln
185 190 195
Lys Ile Thr Leu Ile Gln His Gln Arg Val His Thr Gly Glu Lys
200 205 210
Pro Tyr Glu Cys Lys Val Cys Gly Lys Thr Phe Ser Trp Cys Gly
215 220 225
Arg Phe Ile Leu His Gln Lys Leu His Thr Gln Lys Thr Pro Val
230 235 240
Gln Ala

<210> 187
<211> 194
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature

<223> Incyte ID No: LG:7689661.4.orf2:2002JAN18

<400> 187
Asn Val Lys Glu Cys Gly Lys Ala Phe Arg Val Arg Gly Gln Leu
1 5 10 15
Thr Leu His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys
20 25 30
Lys Glu Cys Gly Lys Thr Phe Ser Arg Gly Tyr His Leu Ile Leu
35 40 45
His His Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu
50 55 60
Cys Trp Lys Ala Phe Ser Arg Tyr Ser Gln Leu Ile Ser His Gln
65 70 75
Ser Ile His Ile Gly Val Lys Pro Tyr Asp Cys Lys Glu Cys Gly
80 85 90
Lys Ala Phe Arg Leu Leu Ser Gln Leu Thr Gln His Gln Ser Ile
95 100 105
His Ile Gly Glu Lys Pro Tyr Lys Cys Lys Glu Cys Gly Lys Ala
110 115 120
Phe Arg Leu Arg Gln Lys Leu Thr Leu His Gln Ser Ile His Thr
125 130 135
Gly Glu Lys Pro Phe Glu Cys Lys Glu Cys Arg Lys Ala Phe Arg
140 145 150
Leu Asn Ser Ser Leu Ile Gln His Leu Arg Ile His Ser Gly Glu
155 160 165
Lys Pro Tyr Glu Cys Lys Glu Cys Lys Lys Ala Phe Arg Gln His
170 175 180
Ser His Leu Thr His His Leu Lys Ile His Asn Val Lys Ile
185 190

<210> 188
<211> 149
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:7690373.1.orf1:2002JAN18

<400> 188
Lys Asn Ser Tyr Trp Arg Lys Asn Pro Thr Asn Met Lys Asn Val
1 5 10 15
Ala Lys Leu Leu Ile Asn Ser Gln Arg Leu Leu Asn Ile Arg Glu
20 25 30
Phe Val Gln Glu Gly Asn Pro Thr Asn Leu Lys Asn Val Ala Ser
35 40 45
Leu Leu Ala Ile Pro Gln Ser Leu Leu Asn Ile His Val Ile His
50 55 60
Thr Gly Gly Asn Ser Tyr Asn Cys Val Glu Cys Cys Asn Ala Leu
65 70 75
Asn Gln Ser Leu Arg Leu Thr Thr Tyr Lys Thr Thr His Thr Gly
80 85 90
Glu Lys Pro Cys Met Cys Glu Glu Cys Gly Lys Ala Ser Asn Arg
95 100 105
Ser Ser Ile Leu Lys Arg His Lys Leu Ile His Thr Gln Glu Arg
110 115 120
Leu Tyr Lys Pro Glu Arg Cys Asp Asn Ala Phe Gly Asn Thr Ser
125 130 135
Asp Phe Ser Glu Tyr Lys Arg Asn Arg Thr Asp Glu Lys Ser
140 145

<210> 189
<211> 268

<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:7696560.1.orf3:2002JAN18

<400> 189
Lys Val Ala Thr Met Arg Lys Leu Phe Ser Phe Gly Arg Arg Leu
1 5 10 15
Gly Gln Ala Leu Leu Asp Ser Met Asp Gln Glu Tyr Ala Gly Arg
20 25 30
Gly Tyr His Ile Arg Asp Trp Glu Leu Arg Lys Ile His Arg Ala
35 40 45
Ala Ile Lys Gly Asp Ala Ala Glu Val Glu His Cys Leu Thr Arg
50 55 60
Arg Phe Arg Asp Leu Asp Ala Arg Asp Arg Lys Asp Arg Thr Val
65 70 75
Leu His Leu Thr Cys Ala His Gly Arg Val Glu Val Val Thr Leu
80 85 90
Leu Leu Ser Arg Arg Cys Gln Ile Asn Ile Tyr Asp Arg Leu Asn
95 100 105
Arg Thr Pro Leu Met Lys Ala Val His Cys Gln Glu Glu Ala Cys
110 115 120
Ala Ile Ile Leu Leu Glu His Gly Ala Asn Pro Asn Ile Lys Asp
125 130 135
Ile Tyr Ser Asn Thr Ala Leu His Tyr Ala Val Tyr Asn Lys Gly
140 145 150
Thr Ser Leu Ala Glu Lys Leu Leu Ser His His Ala Asn Ile Glu
155 160 165
Ala Leu Asn Glu Glu Gly Asn Thr Pro Leu Leu Phe Ala Ile Asn
170 175 180
Ser Arg Arg Gln Gln Ile Val Glu Phe Leu Leu Lys Asn Gln Ala
185 190 195
Asn Leu His Ala Ile Asp Asn Phe Arg Arg Thr Ala Leu Met Leu
200 205 210
Ala Val Gln His Asn Ser Ser Ser Ile Val Ser Leu Leu Leu Gln
215 220 225
Gln Asn Ile Asn Ile Phe Ser Gln Asp Leu Phe Gly Gln Thr Ala
230 235 240
Glu Asp Tyr Ala Val Cys Tyr Asn Phe Arg Ser Ile Gln Gln Gln
245 250 255
Ile Leu Glu His Lys Asn Lys Ile Leu Lys Ser His Leu
260 265

<210> 190
<211> 1304
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:7698190.26.orf3:2002JAN18

<220>
<221> unsure
<222> (1) ... (1304)
<223> unknown or other

<400> 190
Arg Trp Arg Lys Leu Pro Lys Met Pro Glu Ala Val Gly Thr Asp
1 5 10 15
Pro Ser Thr Ser Arg Lys Met Ala Glu Leu Glu Glu Val Thr Leu

20 25 30
Asp Gly Lys Pro Leu Gln Ala Leu Arg Val Thr Asp Leu Lys Ala
35 40 45
Ala Leu Glu Gln Arg Gly Leu Ala Lys Ser Gly Gln Lys Ser Ala
50 55 60
Leu Val Lys Arg Leu Lys Gly Ala Leu Met Leu Glu Asn Leu Gln
65 70 75
Lys His Ser Thr Pro His Ala Ala Phe Gln Pro Asn Ser Gln Ile
80 85 90
Gly Glu Glu Met Ser Gln Asn Ser Phe Ile Lys Gln Tyr Leu Glu
95 100 105
Lys Gln Gln Glu Leu Leu Arg Gln Arg Leu Glu Arg Glu Ala Arg
110 115 120
Glu Ala Ala Glu Leu Glu Glu Ala Ser Ala Glu Ser Glu Asp Glu
125 130 135
Met Ile His Pro Glu Gly Val Ala Ser Leu Leu Pro Pro Asp Phe
140 145 150
Gln Ser Ser Leu Glu Arg Pro Glu Leu Glu Leu Ser Arg His Ser
155 160 165
Pro Arg Lys Ser Ser Ser Ile Ser Glu Glu Lys Gly Asp Ser Asp
170 175 180
Asp Glu Lys Pro Arg Lys Gly Glu Arg Arg Ser Ser Arg Val Arg
185 190 195
Gln Ala Arg Ala Ala Lys Leu Ser Glu Gly Ser Gln Pro Ala Glu
200 205 210
Glu Glu Glu Asp Gln Glu Thr Pro Ser Arg Asn Leu Arg Val Arg
215 220 225
Ala Asp Arg Asn Leu Lys Thr Glu Glu Glu Glu Glu Glu Glu Asp
230 235 240
Gly Gly Gly Thr Lys Ile Asp Glu Glu Glu Gly Asp Asp Glu Gly
245 250 255
Gln Lys Ser Arg Glu Ala Pro Ile Leu Lys Glu Phe Lys Glu Glu
260 265 270
Gly Glu Glu Met Pro Arg Val Lys Pro Glu Glu Met Met Asp Glu
275 280 285
Arg Pro Lys Thr Arg Ser Gln Glu Gln Glu Val Leu Glu Arg Gly
290 295 300
Gly Arg Phe Thr Arg Ser Gln Glu Glu Ala Arg Lys Ser His Leu
305 310 315
Ala Arg Gln Gln Gln Glu Lys Glu Met Lys Thr Thr Ser Pro Leu
320 325 330
Glu Glu Glu Glu Arg Glu Ile Lys Ser Ser Gln Gly Leu Lys Glu
335 340 345
Lys Ser Lys Ser Pro Ser Pro Pro Arg Leu Thr Glu Asp Arg Lys
350 355 360
Lys Ala Ser Leu Val Ala Leu Pro Glu Gln Thr Ala Ser Glu Glu
365 370 375
Glu Thr Pro Pro Pro Leu Leu Thr Lys Glu Ala Ser Ser Pro Pro
380 385 390
Pro His Pro Gln Leu His Ser Glu Glu Glu Ile Glu Pro Met Glu
395 400 405
Gly Pro Ala Pro Pro Val Leu Ile Gln Leu Ser Pro Pro Asn Thr
410 415 420
Asp Ala Asp Thr Arg Glu Leu Leu Val Ser Gln His Thr Val Gln
425 430 435
Leu Val Gly Gly Leu Ser Pro Leu Ser Ser Pro Ser Asp Thr Lys
440 445 450
Ala Glu Ser Pro Ala Glu Lys Val Pro Glu Glu Ser Val Leu Pro
455 460 465
Leu Val Gln Lys Ser Thr Leu Ala Asp Tyr Ser Ala Gln Lys Asp
470 475 480
Leu Glu Pro Glu Ser Asp Arg Ser Ala Gln Pro Leu Pro Leu Lys
485 490 495

Ile Glu Glu Leu Ala Leu Ala Lys Gly Ile Thr Glu Glu Cys Leu
500 505 510
Lys Gln Pro Ser Leu Glu Gln Lys Glu Gly Arg Arg Ala Ser His
515 520 525
Thr Leu Leu Pro Ser His Arg Leu Lys Gln Ser Ala Asp Ser Ser
530 535 540
Ser Ser Arg Ser Ser Ser Ser Ser Ser Ser Ser Ser Arg Ser Arg
545 550 555
Ser Arg Ser Pro Asp Ser Ser Gly Ser Arg Ser His Ser Pro Leu
560 565 570
Arg Ser Lys Gln Arg Asp Val Ala Gln Ala Arg Thr His Ala Asn
575 580 585
Pro Arg Gly Arg Pro Lys Met Gly Ser Arg Ser Thr Ser Glu Ser
590 595 600
Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Ala Ser Ser Asn Ser
605 610 615
Arg Lys Ser Leu Ser Pro Gly Val Ser Arg Asp Ser Ser Thr Ser
620 625 630
Tyr Thr Glu Thr Lys Asp Pro Ser Ser Gly Gln Glu Val Ala Thr
635 640 645
Pro Pro Val Pro Gln Leu Gln Val Cys Glu Pro Lys Glu Arg Thr
650 655 660
Ser Thr Ser Ser Ser Ser Val Gln Ala Arg Arg Leu Ser Gln Pro
665 670 675
Glu Ser Ala Glu Lys His Val Thr Gln Arg Leu Gln Pro Glu Arg
680 685 690
Gly Ser Pro Lys Lys Cys Glu Ala Glu Glu Ala Glu Pro Pro Ala
695 700 705
Ala Thr Gln Pro Gln Thr Ser Glu Thr Gln Thr Ser His Leu Pro
710 715 720
Glu Ser Glu Arg Ile His His Thr Val Glu Glu Lys Glu Glu Val
725 730 735
Thr Met Asp Thr Ser Glu Asn Arg Pro Glu Asn Asp Val Pro Glu
740 745 750
Pro Pro Met Pro Ile Ala Asp Gln Val Ser Asn Asp Asp Arg Pro
755 760 765
Glu Gly Ser Val Glu Asp Glu Glu Lys Lys Glu Ser Ser Leu Pro
770 775 780
Lys Ser Phe Lys Arg Lys Ile Ser Val Val Ser Ala Thr Lys Gly
785 790 795
Val Pro Ala Gly Asn Ser Asp Thr Glu Gly Gly Gln Pro Gly Arg
800 805 810
Lys Arg Arg Trp Gly Ala Ser Thr Ala Thr Thr Gln Lys Lys Pro
815 820 825
Ser Ile Ser Ile Thr Thr Glu Ser Leu Lys Ser Leu Ile Pro Asp
830 835 840
Ile Lys Pro Leu Ala Gly Gln Glu Ala Val Val Asp Leu His Ala
845 850 855
Asp Asp Ser Arg Ile Ser Glu Asp Glu Thr Glu Arg Asn Gly Asp
860 865 870
Asp Gly Thr His Asp Lys Gly Leu Lys Ile Cys Arg Thr Val Thr
875 880 885
Gln Val Val Pro Ala Glu Gly Gln Glu Asn Gly Gln Arg Glu Glu
890 895 900
Glu Glu Glu Glu Lys Glu Pro Glu Ala Glu Pro Pro Val Pro Pro
905 910 915
Gln Val Ser Val Glu Val Ala Leu Pro Pro Pro Ala Glu His Glu
920 925 930
Val Lys Lys Val Thr Leu Gly Asp Thr Leu Thr Arg Arg Ser Ile
935 940 945
Ser Gln Gln Lys Ser Gly Val Ser Ile Thr Ile Asp Asp Pro Val
950 955 960
Arg Thr Ala Gln Val Pro Ser Pro Pro Arg Gly Lys Ile Ser Asn

965 970 975
Ile Val His Ile Ser Asn Leu Val Arg Pro Phe Thr Leu Gly Gln
980 985 990
Leu Lys Glu Leu Leu Gly Arg Thr Gly Thr Leu Val Glu Glu Ala
995 1000 1005
Phe Trp Ile Asp Lys Ile Lys Ser His Cys Phe Val Thr Tyr Ser
1010 1015 1020
Thr Val Glu Glu Ala Val Ala Thr Arg Thr Ala Leu His Gly Val
1025 1030 1035
Lys Trp Pro Gln Ser Asn Pro Lys Phe Leu Cys Ala Asp Tyr Ala
1040 1045 1050
Glu Gln Asp Glu Leu Asp Tyr His Arg Gly Leu Leu Val Asp Arg
1055 1060 1065
Pro Ser Glu Thr Lys Thr Glu Glu Gln Gly Ile Pro Arg Pro Leu
1070 1075 1080
His Pro Pro Pro Pro Pro Pro Val Gln Pro Pro Gln His Pro Arg
1085 1090 1095
Ala Glu Gln Arg Glu Gln Glu Arg Ala Val Arg Glu Gln Trp Ala
1100 1105 1110
Glu Arg Glu Arg Glu Met Glu Arg Arg Glu Arg Thr Arg Ser Glu
1115 1120 1125
Arg Glu Trp Asp Arg Asp Lys Val Arg Glu Gly Pro Arg Ser Arg
1130 1135 1140
Ser Arg Ser Arg Asp Arg Arg Arg Lys Glu Arg Ala Lys Ser Lys
1145 1150 1155
Glu Lys Lys Ser Glu Lys Lys Glu Lys Ala Gln Glu Glu Pro Pro
1160 1165 1170
Ala Lys Leu Leu Asp Asp Leu Phe Arg Lys Thr Lys Ala Ala Pro
1175 1180 1185
Cys Ile Tyr Trp Leu Pro Leu Thr Asp Ser Gln Ile Val Gln Lys
1190 1195 1200
Glu Ala Glu Arg Ala Glu Arg Ala Lys Glu Arg Glu Lys Arg Arg
1205 1210 1215
Lys Glu Gln Glu Glu Glu Glu Gln Lys Glu Arg Glu Lys Glu Ala
1220 1225 1230
Glu Arg Glu Arg Asn Arg Gln Leu Glu Arg Glu Lys Arg Arg Glu
1235 1240 1245
His Ser Arg Glu Arg Asp Arg Xaa Arg Xaa Arg Glu Arg Glu Arg
1250 1255 1260
Asp Arg Gly Asp Arg Asp Arg Asp Arg Glu Arg Asp Arg Glu Arg
1265 1270 1275
Gly Arg Glu Arg Asp Arg Arg Asp Thr Lys Arg His Ser Arg Ser
1280 1285 1290
Arg Ser Arg Ser Thr Pro Val Arg Asp Arg Gly Gly Arg Arg
1295 1300

<210> 191
<211> 239
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:7763560.12.orf1:2002JAN18

<220>
<221> unsure
<222> (1) ... (239)
<223> unknown or other

<400> 191
Ser Arg Cys Xaa Val Thr Arg Gly Ser Gln Ala Trp Leu Pro Leu
1 5 10 15

Leu Phe Thr Pro Leu Tyr Glu Ser Ser His Leu Glu Arg Pro Ala
20 25 30
Leu Arg Pro Met Val Ala Ala Arg Trp Gly Ala Thr Val Gly Pro
35 40 45
Gly Ala Val Trp Thr Gln Cys Tyr Gly Trp Gly Trp Pro Glu Pro
50 55 60
Ala Trp Asp Ser Arg Glu Trp Arg Arg Val Val Gly Pro Gly Lys
65 70 75
Arg Pro Arg Leu Leu Ala His Pro Leu Trp Ala Ser Leu Glu Leu
80 85 90
Leu Phe Leu Val Ser Gln Glu Asp Thr Leu Ser Pro Gly Ala Val
95 100 105
Gly Pro Arg Cys Val Gly Asp Pro Gly Ser Ala Leu Gly Pro Leu
110 115 120
His Val Gly Asp Thr Gly Asn Ala Arg Ser Pro Pro Cys Phe Ser
125 130 135
Pro His Leu Pro Ile Ser Thr Cys Gly Ala Arg Gly Ser Asp Pro
140 145 150
Lys Ala Ala Ser His Pro Pro Ser Pro Ala Pro Pro Ala Leu Arg
155 160 165
Ala Gln Gly Ala Ala Gln Pro Cys His Leu Cys Ser Ser Pro Ala
170 175 180
Pro His Thr Asn Leu Gly Pro Gly Gly Pro Ala His Pro Gly Leu
185 190 195
Arg Arg Pro Pro Pro Leu Val His Met Ala Ser Pro Ser Cys Arg
200 205 210
Gly Ser Gly Cys Cys Pro His Arg Ala Gly Ser Leu Leu Arg Cys
215 220 225
Ala Gly Lys Ala Gly Trp Cys Arg Gly Ala Arg Arg Gly Arg
230 235

<210> 192
<211> 837
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:7763587.20.orf2:2002JAN18

<400> 192
Pro Ala Leu Leu Ser Leu Val Leu Pro Ser Gln Gly Glu Ala Pro
1 5 10 15
Ala Glu Met Gly Ala Leu Leu Leu Glu Lys Glu Thr Arg Gly Ala
20 25 30
Thr Glu Arg Val His Gly Ser Leu Gly Asp Thr Pro Arg Ser Glu
35 40 45
Glu Thr Leu Pro Lys Ala Thr Pro Asp Ser Leu Glu Pro Ala Gly
50 55 60
Pro Ser Ser Pro Ala Ser Val Thr Val Thr Val Gly Asp Glu Gly
65 70 75
Ala Asp Thr Pro Val Gly Ala Thr Pro Leu Ile Gly Asp Glu Ser
80 85 90
Glu Asn Leu Glu Gly Asp Gly Asp Leu Arg Gly Gly Arg Ile Leu
95 100 105
Leu Gly His Ala Thr Lys Ser Phe Pro Ser Ser Pro Ser Lys Gly
110 115 120
Gly Ser Cys Pro Ser Arg Ala Lys Met Ser Met Thr Gly Ala Gly
125 130 135
Lys Ser Pro Pro Ser Val Gln Ser Leu Ala Met Arg Leu Leu Ser
140 145 150
Met Pro Gly Ala Gln Gly Ala Ala Ala Ala Gly Ser Glu Pro Pro
155 160 165

Pro Ala Thr Thr Ser Pro Glu Gly Gln Pro Lys Val His Arg Ala
170 175 180
Arg Lys Thr Met Ser Lys Pro Gly Asn Gly Gln Pro Pro Val Pro
185 190 195
Glu Lys Arg Pro Pro Glu Ile Gln His Phe Arg Met Ser Asp Asp
200 205 210
Val His Ser Leu Gly Lys Val Thr Ser Asp Leu Ala Lys Arg Arg
215 220 225
Lys Leu Asn Ser Gly Gly Gly Leu Ser Glu Glu Leu Gly Ser Ala
230 235 240
Arg Arg Ser Gly Glu Val Thr Leu Thr Lys Gly Asp Pro Gly Ser
245 250 255
Leu Glu Glu Trp Glu Thr Val Val Gly Asp Asp Phe Ser Leu Tyr
260 265 270
Tyr Asp Ser Tyr Ser Val Asp Glu Arg Val Asp Ser Asp Ser Lys
275 280 285
Ser Glu Val Glu Ala Leu Thr Glu Gln Leu Ser Glu Glu Glu Glu
290 295 300
Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu
305 310 315
Glu Glu Glu Glu Glu Asp Glu Glu Ser Gly Asn Gln Ser Asp Arg
320 325 330
Ser Gly Ser Ser Gly Arg Arg Lys Ala Lys Lys Lys Trp Arg Lys
335 340 345
Asp Ser Pro Trp Val Lys Pro Ser Arg Lys Arg Arg Lys Arg Glu
350 355 360
Pro Pro Arg Ala Lys Glu Pro Arg Gly Val Ser Asn Asp Thr Ser
365 370 375
Ser Leu Glu Thr Glu Arg Gly Phe Glu Glu Leu Pro Leu Cys Ser
380 385 390
Cys Arg Met Glu Ala Pro Lys Ile Asp Arg Ile Ser Glu Arg Ala
395 400 405
Gly His Lys Cys Met Ala Thr Glu Ser Val Asp Gly Glu Leu Ser
410 415 420
Gly Cys Asn Ala Ala Ile Leu Lys Arg Glu Thr Met Arg Pro Ser
425 430 435
Ser Arg Val Ala Leu Met Val Leu Cys Glu Thr His Arg Ala Arg
440 445 450
Met Val Lys His His Cys Cys Pro Gly Cys Gly Tyr Phe Cys Thr
455 460 465
Ala Gly Thr Phe Leu Glu Cys His Pro Asp Phe Arg Val Ala His
470 475 480
Arg Phe His Lys Ala Cys Val Ser Gln Leu Asn Gly Met Val Phe
485 490 495
Cys Pro His Cys Gly Glu Asp Ala Ser Glu Ala Gln Glu Val Thr
500 505 510
Ile Pro Arg Gly Asp Gly Val Thr Pro Pro Ala Gly Thr Ala Ala
515 520 525
Pro Ala Pro Pro Pro Leu Ser Gln Asp Val Pro Gly Arg Ala Asp
530 535 540
Thr Ser Gln Pro Ser Ala Arg Met Arg Gly His Gly Glu Pro Arg
545 550 555
Arg Pro Pro Cys Asp Pro Leu Ala Asp Thr Ile Asp Ser Ser Gly
560 565 570
Pro Ser Leu Thr Leu Pro Asn Gly Gly Cys Leu Ser Ala Val Gly
575 580 585
Leu Pro Leu Gly Pro Gly Arg Glu Ala Leu Glu Lys Ala Leu Val
590 595 600
Ile Gln Glu Ser Glu Arg Arg Lys Lys Leu Arg Phe His Pro Arg
605 610 615
Gln Leu Tyr Leu Ser Val Lys Gln Gly Glu Leu Gln Lys Val Ile
620 625 630
Leu Met Leu Leu Asp Asn Leu Asp Pro Asn Phe Gln Ser Asp Gln

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                635                     640                     645
Gln Ser Lys Arg Thr Pro Leu His Ala Ala Ala Gln Lys Gly Ser
                650                     655                     660
Val Glu Ile Cys His Val Leu Leu Gln Ala Gly Ala Asn Ile Asn
                665                     670                     675
Ala Val Asp Lys Gln Gln Arg Thr Pro Leu Met Glu Ala Val Val
                680                     685                     690
Asn Asn His Leu Glu Val Ala Arg Tyr Met Val Gln Arg Gly Gly
                695                     700                     705
Cys Val Tyr Ser Lys Glu Glu Asp Gly Ser Thr Cys Leu His His
                710                     715                     720
Ala Ala Lys Ile Gly Asn Leu Glu Met Val Ser Leu Leu Leu Ser
                725                     730                     735
Thr Gly Gln Val Asp Val Asn Ala Gln Asp Ser Gly Gly Trp Thr
                740                     745                     750
Pro Ile Ile Trp Ala Ala Glu His Lys His Ile Glu Val Ile Arg
                755                     760                     765
Met Leu Leu Thr Arg Gly Ala Asp Val Thr Leu Thr Asp Asn Val
                770                     775                     780
Ser Glu Arg Leu Val Glu Val Gly Gln Pro Gln Ala Pro Glu Gln
                785                     790                     795
Gly Gly Gly Trp Ile Gln Gly Pro Ser Cys Cys Thr Ser Ser Val
                800                     805                     810
Pro Leu Leu Pro Pro Gln Glu Glu Asn Ile Cys Leu His Trp Ala
                815                     820                     825
Ser Phe Thr Gly Ser Ala Ala Ile Ala Glu Val Leu
                830                     835
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<210> 193
<211> 445
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:899263.10.orf2:2002JAN18

<400> 193

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Leu Lys His Gly Ile Ser Asp Val Thr Cys Pro Lys Trp His Ser
 1              5                   10                  15
Arg Leu Ile Asn Gly Leu Gly Cys Lys Leu Ser Phe Ile Pro Trp
                20                  25                  30
Asp Ala Leu Ser Ala Leu Gln His Leu Lys Phe Arg Gln Arg Glu
                35                  40                  45
Leu Thr Trp Gly Gln Ala Ala Pro Leu Gly Arg Val Glu Asp Arg
                50                  55                  60
Val Ser Leu Leu Ile Phe Arg Lys Ser Ser Arg Thr Gln Ser Pro
                65                  70                  75
Ala Phe Gly Ser Leu Ser Gln Arg Asp Arg Arg Asn Pro Glu Gln
                80                  85                  90
Ala Thr Gly Arg Arg Ser Gly Met Tyr Phe Cys Trp Gly Ala Asp
                95                  100                 105
Ser Arg Glu Leu Gln Arg Arg Arg Thr Ala Gly Ser Pro Gly Ala
                110                 115                 120
Glu Leu Leu Gln Ala Ala Ser Gly Glu Arg His Ser Leu Leu Leu
                125                 130                 135
Leu Thr Asn His Arg Val Leu Ser Cys Gly Asp Asn Ser Arg Gly
                140                 145                 150
Gln Leu Gly Arg Arg Gly Ala Gln Arg Gly Glu Leu Pro Glu Pro
                155                 160                 165
Ile Gln Ala Leu Glu Thr Leu Ile Val Asp Leu Val Ser Cys Gly
                170                 175                 180
Lys Glu His Ser Leu Ala Val Cys His Lys Gly Arg Val Phe Ala
```

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                    185                     190                     195
Trp Gly Ala Gly Ser Glu Gly Gln Leu Gly Ile Gly Glu Phe Lys
                200                 205                 210
Glu Ile Ser Phe Thr Pro Lys Lys Ile Met Thr Leu Asn Asp Ile
                215                 220                 225
Lys Ile Ile Gln Val Ser Cys Gly His Tyr His Ser Leu Ala Leu
                230                 235                 240
Ser Lys Asp Ser Gln Val Phe Ser Trp Gly Lys Asn Ser His Gly
                245                 250                 255
Gln Leu Gly Leu Gly Lys Glu Phe Pro Ser Gln Ala Ser Pro Gln
                260                 265                 270
Arg Val Arg Ser Leu Glu Gly Ile Pro Leu Ala Gln Val Ala Ala
                275                 280                 285
Gly Gly Ala His Ser Phe Ala Leu Ser Leu Cys Gly Thr Ser Phe
                290                 295                 300
Gly Trp Gly Ser Asn Ser Ala Gly Gln Leu Ala Leu Ser Gly Arg
                305                 310                 315
Asn Val Pro Val Gln Ser Asn Lys Pro Leu Ser Val Gly Ala Leu
                320                 325                 330
Lys Asn Leu Gly Val Val Tyr Ile Ser Cys Gly Asp Ala His Thr
                335                 340                 345
Ala Val Leu Thr Gln Asp Gly Lys Val Phe Thr Phe Gly Asp Asn
                350                 355                 360
Arg Ser Gly Gln Leu Gly Tyr Ser Pro Thr Pro Glu Lys Arg Gly
                365                 370                 375
Pro Gln Leu Val Glu Arg Ile Asp Gly Leu Val Ser Gln Ile Asp
                380                 385                 390
Cys Gly Ser Tyr His Thr Leu Ala Tyr Val His Thr Thr Gly Gln
                395                 400                 405
Val Val Ser Phe Gly His Gly Pro Ser Asp Thr Ser Lys Pro Thr
                410                 415                 420
His Pro Glu Ala Leu Thr Glu Asn Phe Asp Ile Ser Cys Leu Ile
                425                 430                 435
Ser Ala Glu Glu Thr Leu Ser Met Asp Leu
                440                 445

<210> 194
<211> 139
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:977837.31.orf1:2002JAN18

<400> 194
Phe Thr Cys Arg Asn Leu His Phe Ile Gln Asn Lys Leu Asn Val
 1               5                  10                  15
Ile Thr Leu Leu Arg His Leu Asn Thr Ser Ser Leu Leu Cys Asp
                20                  25                  30
Cys Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe
                35                  40                  45
Gln Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys
                50                  55                  60
Gly Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp
                65                  70                  75
Asp Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser
                80                  85                  90
Ala Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser
                95                 100                 105
Ser Ser Asp Ser Pro Met Thr Leu Leu Gly Lys Lys Thr Met Asn
               110                 115                 120
Tyr Cys Met Met Leu Lys Trp Lys Ile Met His Thr Ser Gly Pro
```

125 130 135
Lys Val Ala Arg

<210> 195
<211> 650
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:978560.13.orf2:2002JAN18

<400> 195
Leu Pro Phe Ser Glu Asp Gly Ser Ser Val Pro His Ile Cys His
1 5 10 15
Val His Pro Gly Phe His Leu Ser Pro Gly Leu Arg Ile Ser Cys
20 25 30
Phe Phe Lys Arg Pro Phe Leu Ser Pro Glu Phe Gly Pro Val Arg
35 40 45
Val Gln Trp Ser Gly Ala Ser His Thr Gln Cys Trp Phe Pro Gly
50 55 60
Ile Gly Asp Phe Pro Arg Cys Arg Cys Gly Leu Tyr Arg Glu Gly
65 70 75
Val Ala Leu Ala Gly Phe Phe Ser Glu Lys Thr Val Gln Arg Cys
80 85 90
Asn Ala Gly Glu Leu Gln Gln Pro His Phe Thr Gly Asn Phe Gly
95 100 105
Thr Thr His Phe Ala Ala Pro Lys Ser Asp Leu Ser Thr Leu Arg
110 115 120
Ser Ile Glu Asp Pro Ser Val Glu Pro Arg Leu Leu Glu Gly Val
125 130 135
Val Pro Leu His Gly Pro Pro Ser Thr Cys Val Phe Pro Val Ser
140 145 150
Val Gly Tyr Gln Val Gly Lys Pro Ser Leu Ile Ser His Leu Glu
155 160 165
Gln Glu Glu Glu Pro Arg Thr Glu Glu Arg Gly Ala His Gln Gly
170 175 180
Ala Cys Ala Asp Trp Glu Thr Pro Ser Lys Thr Lys Trp Ser Leu
185 190 195
Leu Met Glu Asp Ile Phe Gly Lys Glu Thr Pro Ser Gly Val Thr
200 205 210
Met Glu Arg Ala Gly Leu Gly Glu Lys Ser Thr Glu Tyr Ala His
215 220 225
Leu Phe Glu Val Phe Gly Met Asp Pro His Leu Thr Gln Pro Met
230 235 240
Gly Arg His Ala Gly Lys Arg Pro Tyr His Arg Arg Asp Tyr Gly
245 250 255
Val Ala Phe Lys Gly Arg Pro His Leu Thr Gln His Met Ser Met
260 265 270
Tyr Asp Gly Arg Lys Met His Glu Cys His Gln Cys Gln Lys Ala
275 280 285
Phe Thr Thr Ser Ala Ser Leu Thr Arg His Arg Arg Ile His Thr
290 295 300
Gly Glu Lys Pro Tyr Glu Cys Ser Asp Cys Gly Lys Ala Phe Asn
305 310 315
Asp Pro Ser Ala Leu Arg Ser His Ala Arg Thr His Leu Lys Glu
320 325 330
Lys Pro Phe Asp Cys Ser Gln Cys Gly Asn Ala Phe Arg Thr Leu
335 340 345
Ser Ala Leu Lys Ile His Met Arg Val His Thr Gly Glu Arg Pro
350 355 360
Tyr Lys Cys Asp Gln Cys Gly Lys Ala Tyr Gly Arg Ser Cys His

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                    365                           370                           375
Leu Ile Ala His Lys Arg Thr His Thr Gly Glu Arg Pro Tyr Glu
                    380                           385                           390
Cys His Asp Cys Gly Lys Ala Phe Gln His Pro Ser His Leu Lys
                    395                           400                           405
Glu His Val Arg Asn His Thr Gly Glu Lys Pro Tyr Ala Cys Thr
                    410                           415                           420
Gln Cys Gly Lys Ala Phe Arg Trp Lys Ser Asn Phe Asn Leu His
                    425                           430                           435
Lys Lys Asn His Met Val Glu Lys Thr Tyr Glu Cys Lys Glu Cys
                    440                           445                           450
Gly Lys Ser Phe Gly Asp Leu Val Ser Arg Arg Lys His Met Arg
                    455                           460                           465
Ile His Ile Val Lys Lys Pro Val Glu Cys Arg Gln Cys Gly Lys
                    470                           475                           480
Thr Phe Arg Asn Gln Ser Ile Leu Lys Thr His Met Asn Ser His
                    485                           490                           495
Thr Gly Glu Lys Pro Tyr Gly Cys Asp Leu Cys Gly Lys Ala Phe
                    500                           505                           510
Ser Ala Ser Ser Asn Leu Thr Ala His Arg Lys Ile His Thr Gln
                    515                           520                           525
Glu Arg Arg Tyr Glu Cys Ala Ala Cys Gly Lys Val Phe Gly Asp
                    530                           535                           540
Tyr Leu Ser Arg Arg Arg His Met Ser Val His Leu Val Lys Lys
                    545                           550                           555
Arg Val Glu Cys Arg Gln Cys Gly Lys Ala Phe Arg Asn Gln Ser
                    560                           565                           570
Thr Leu Lys Thr His Met Arg Ser His Thr Gly Glu Lys Pro Tyr
                    575                           580                           585
Glu Cys Asp His Cys Gly Lys Ala Phe Ser Ile Gly Ser Asn Leu
                    590                           595                           600
Asn Val His Arg Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys
                    605                           610                           615
Leu Val Cys Gly Lys Ala Phe Ser Asp His Ser Ser Leu Arg Ser
                    620                           625                           630
His Val Lys Thr His Arg Gly Glu Lys Leu Phe Val Ser Ser Val
                    635                           640                           645
Trp Lys Arg Leu Gln
                    650
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<210> 196
<211> 157
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:979390.2.orf1:2002JAN18

<400> 196

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Asn Ser Leu Ser Val Ala Ser Ala Pro Pro Gln Arg Asp Pro Gly
 1               5                  10                  15
Met Ala Met Ala Leu Pro Met Pro Gly Pro Gln Glu Ala Val Val
                20                  25                  30
Phe Glu Asp Val Ala Val Tyr Phe Thr Arg Ile Glu Trp Ser Cys
                35                  40                  45
Leu Ala Pro Asp Gln Gln Ala Leu Tyr Arg Asp Val Met Leu Glu
                50                  55                  60
Asn Tyr Gly Asn Leu Ala Ser Leu Gly Phe Leu Val Ala Lys Pro
                65                  70                  75
Ala Leu Ile Ser Leu Leu Glu Gln Gly Glu Glu Pro Gly Ala Leu
                80                  85                  90
Ile Leu Gln Val Ala Glu Gln Ser Val Ala Lys Ala Ser Leu Cys
```

95 100 105
Thr Glu Asp Pro Asn Thr Leu Pro Ser Arg Ser Gln Glu Gly Ser
110 115 120
Pro Ala Ser Ser Glu Gly Gly Pro Gly Glu Lys Gly Val Ala Gly
125 130 135
Arg Val Ala Gly Gly Gly Ala Ala Ser Ser Trp Pro His Gly Glu
140 145 150
His Pro Val Thr Pro Asn Arg
155

<210> 197
<211> 431
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:983019.1.orf2:2002JAN18

<400> 197
Arg Leu Trp Leu Lys Phe His Arg His Gln Thr Glu Met Ile Ile
1 5 10 15
Thr Lys Gln Gly Arg Arg Met Phe Pro Phe Leu Ser Phe Asn Ile
20 25 30
Asn Gly Leu Asn Pro Thr Ala His Tyr Asn Val Phe Val Glu Val
35 40 45
Val Leu Ala Asp Pro Asn His Trp Arg Phe Gln Gly Gly Lys Trp
50 55 60
Val Thr Cys Gly Lys Ala Asp Asn Asn Met Gln Gly Asn Lys Met
65 70 75
Tyr Val His Pro Glu Ser Pro Asn Thr Gly Ser His Trp Met Arg
80 85 90
Gln Glu Ile Ser Phe Gly Lys Leu Lys Leu Thr Asn Asn Lys Gly
95 100 105
Ala Asn Asn Asn Asn Thr Gln Met Ile Val Leu Gln Ser Leu His
110 115 120
Lys Tyr Gln Pro Arg Leu His Ile Val Glu Val Thr Glu Asp Gly
125 130 135
Val Glu Asp Leu Asn Glu Pro Ser Lys Thr Gln Thr Phe Thr Phe
140 145 150
Ser Glu Thr Gln Phe Ile Ala Val Thr Ala Tyr Gln Asn Thr Asp
155 160 165
Ile Thr Gln Leu Lys Ile Asp His Asn Pro Phe Ala Lys Gly Phe
170 175 180
Arg Asp Asn Tyr Asp Ser Met Tyr Thr Ala Ser Glu Asn Asp Arg
185 190 195
Leu Thr Pro Ser Pro Thr Asp Ser Pro Arg Ser His Gln Ile Val
200 205 210
Pro Gly Gly Arg Tyr Gly Val Gln Ser Phe Phe Pro Glu Pro Phe
215 220 225
Val Asn Thr Leu Pro Gln Ala Arg Tyr Tyr Asn Gly Glu Arg Thr
230 235 240
Val Pro Gln Thr Asn Gly Leu Leu Ser Pro Gln Gln Ser Glu Glu
245 250 255
Val Ala Asn Pro Pro Gln Arg Trp Leu Val Thr Pro Val Gln Gln
260 265 270
Pro Gly Thr Asn Lys Leu Asp Ile Ser Ser Tyr Glu Ser Glu Tyr
275 280 285
Thr Ser Ser Thr Leu Leu Pro Tyr Gly Ile Lys Ser Leu Pro Leu
290 295 300
Gln Thr Ser His Ala Leu Gly Tyr Tyr Pro Asp Pro Thr Phe Pro
305 310 315
Ala Met Ala Gly Trp Gly Gly Arg Gly Ser Tyr Gln Arg Lys Met

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                320                        325                        330
Ala Ala Gly Leu Pro Trp Thr Ser Arg Thr Ser Pro Thr Val Phe
                335                        340                        345
Ser Glu Asp Gln Leu Ser Lys Glu Lys Val Lys Glu Glu Ile Gly
                350                        355                        360
Ser Ser Trp Ile Glu Thr Pro Pro Ser Ile Lys Ser Leu Asp Ser
                365                        370                        375
Asn Asp Ser Gly Val Tyr Thr Ser Ala Cys Lys Arg Arg Arg Leu
                380                        385                        390
Ser Pro Ser Asn Ser Ser Asn Glu Asn Ser Pro Ser Ile Lys Cys
                395                        400                        405
Glu Asp Ile Asn Ala Glu Glu Tyr Ser Lys Asp Thr Ser Lys Gly
                410                        415                        420
Met Gly Gly Tyr Tyr Ala Phe Tyr Thr Thr Pro
                425                        430

<210> 198
<211> 975
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:997202.7.orf2:2002JAN18

<400> 198
Ser Leu Ser Gly Phe Thr Arg Glu Ala Ser Phe Glu Met Ala Ala
1               5                   10                  15
Gln Arg Ile Arg Ala Ala Asn Ser Asn Gly Leu Pro Arg Cys Lys
                20                  25                  30
Ser Glu Gly Thr Leu Ile Asp Leu Ser Glu Gly Phe Ser Glu Thr
                35                  40                  45
Ser Phe Asn Asp Ile Lys Val Pro Ser Pro Ser Ala Leu Leu Val
                50                  55                  60
Asp Asn Pro Thr Pro Phe Gly Asn Ala Lys Glu Val Ile Ala Ile
                65                  70                  75
Lys Asp Tyr Cys Pro Thr Asn Phe Thr Thr Leu Lys Phe Ser Lys
                80                  85                  90
Gly Asp His Leu Tyr Val Leu Asp Thr Ser Gly Gly Glu Trp Trp
                95                  100                 105
Tyr Ala His Asn Thr Thr Glu Met Gly Tyr Ile Pro Ser Ser Tyr
                110                 115                 120
Val Gln Pro Leu Asn Tyr Arg Asn Ser Thr Leu Ser Asp Ser Gly
                125                 130                 135
Met Ile Asp Asn Leu Pro Asp Ser Pro Asp Glu Val Ala Lys Glu
                140                 145                 150
Leu Glu Leu Leu Gly Gly Trp Thr Asp Asp Lys Lys Val Pro Gly
                155                 160                 165
Arg Met Tyr Ser Asn Asn Pro Phe Trp Asn Gly Val Gln Thr Asn
                170                 175                 180
Pro Phe Leu Asn Gly Asn Val Pro Val Met Pro Ser Leu Asp Glu
                185                 190                 195
Leu Asn Pro Lys Ser Thr Val Asp Leu Leu Leu Phe Asp Ala Gly
                200                 205                 210
Thr Ser Ser Phe Thr Glu Ser Ser Ser Ala Thr Thr Asn Ser Thr
                215                 220                 225
Gly Asn Ile Phe Asp Glu Leu Pro Val Thr Asn Gly Leu His Ala
                230                 235                 240
Glu Pro Pro Val Arg Arg Asp Asn Pro Phe Phe Arg Ser Lys Arg
                245                 250                 255
Ser Tyr Ser Leu Ser Glu Leu Ser Val Leu Gln Ala Lys Ser Asp
                260                 265                 270
Ala Pro Thr Ser Ser Ser Phe Phe Thr Gly Leu Lys Ser Pro Ala
```

275 280 285
Pro Glu Gln Phe Gln Ser Arg Glu Asp Phe Arg Thr Ala Trp Leu
290 295 300
Asn His Arg Lys Leu Ala Arg Ser Cys His Asp Leu Asp Leu Leu
305 310 315
Gly Gln Ser Pro Gly Trp Gly Gln Thr Gln Ala Val Glu Thr Asn
320 325 330
Ile Val Cys Lys Leu Asp Ser Ser Gly Gly Ala Val Gln Leu Pro
335 340 345
Asp Thr Ser Ile Ser Ile His Val Pro Glu Gly His Val Ala Pro
350 355 360
Gly Glu Thr Gln Gln Ile Ser Met Lys Ala Leu Leu Asp Pro Pro
365 370 375
Leu Glu Leu Asn Ser Asp Arg Ser Cys Ser Ile Ser Pro Val Leu
380 385 390
Glu Val Lys Leu Ser Asn Leu Glu Val Lys Thr Ser Ile Ile Leu
395 400 405
Glu Met Lys Val Ser Ala Glu Ile Lys Asn Asp Leu Phe Ser Lys
410 415 420
Ser Thr Val Gly Leu Gln Cys Leu Arg Ser Asp Ser Lys Glu Gly
425 430 435
Pro Tyr Val Ser Val Pro Leu Asn Cys Ser Cys Gly Asp Thr Val
440 445 450
Gln Ala Gln Leu His Asn Leu Glu Pro Cys Met Tyr Val Ala Val
455 460 465
Val Ala His Gly Pro Ser Ile Leu Tyr Pro Ser Thr Val Trp Asp
470 475 480
Phe Ile Asn Lys Lys Val Thr Val Gly Leu Tyr Gly Pro Lys His
485 490 495
Ile His Pro Ser Phe Lys Thr Val Val Thr Ile Phe Gly His Asp
500 505 510
Cys Ala Pro Lys Thr Leu Leu Val Ser Glu Val Thr Arg Gln Ala
515 520 525
Pro Asn Pro Ala Pro Val Ala Leu Gln Leu Trp Gly Lys His Gln
530 535 540
Phe Val Leu Ser Arg Pro Gln Asp Leu Lys Val Cys Met Phe Ser
545 550 555
Asn Met Thr Asn Tyr Glu Val Lys Ala Ser Glu Gln Ala Lys Val
560 565 570
Val Arg Gly Phe Gln Leu Lys Leu Gly Lys Val Ser Arg Leu Ile
575 580 585
Phe Pro Ile Thr Ser Gln Asn Pro Asn Glu Leu Ser Asp Phe Thr
590 595 600
Leu Arg Val Gln Val Lys Asp Asp Gln Glu Ala Ile Leu Thr Gln
605 610 615
Phe Cys Val Gln Thr Pro Gln Pro Pro Pro Lys Ser Ala Ile Lys
620 625 630
Pro Ser Gly Gln Arg Arg Phe Leu Lys Lys Asn Glu Val Gly Lys
635 640 645
Ile Ile Leu Ser Pro Phe Ala Thr Thr Thr Lys Tyr Pro Thr Phe
650 655 660
Gln Asp Arg Pro Val Ser Ser Leu Lys Phe Gly Lys Leu Leu Lys
665 670 675
Thr Val Val Arg Gln Asn Lys Asn His Tyr Leu Leu Glu Tyr Lys
680 685 690
Lys Gly Asp Gly Ile Ala Leu Leu Ser Glu Glu Arg Val Arg Leu
695 700 705
Arg Gly Gln Leu Trp Thr Lys Glu Trp Tyr Ile Gly Tyr Tyr Gln
710 715 720
Gly Arg Val Gly Leu Val His Thr Lys Asn Val Leu Val Val Gly
725 730 735
Arg Ala Arg Pro Ser Leu Cys Ser Gly Pro Glu Leu Ser Thr Ser
740 745 750

Val Leu Leu Glu Gln Ile Leu Arg Pro Cys Lys Phe Leu Thr Tyr
755 760 765
Ile Tyr Ala Ser Val Arg Thr Leu Leu Met Glu Asn Ile Ser Ser
770 775 780
Trp Arg Ser Phe Ala Asp Ala Leu Gly Tyr Val Asn Leu Pro Leu
785 790 795
Thr Phe Phe Cys Arg Ala Glu Leu Asp Ser Glu Pro Glu Arg Val
800 805 810
Ala Ser Val Leu Glu Lys Leu Lys Glu Asp Cys Asn Asn Thr Glu
815 820 825
Asn Lys Glu Arg Lys Ser Phe Gln Lys Glu Leu Val Met Ala Leu
830 835 840
Leu Lys Met Asp Cys Gln Gly Leu Val Val Arg Leu Ile Gln Asp
845 850 855
Phe Val Leu Leu Thr Thr Ala Val Glu Val Ala Gln Arg Trp Arg
860 865 870
Glu Leu Ala Glu Lys Leu Ala Lys Val Ser Lys Gln Gln Met Asp
875 880 885
Ala Tyr Glu Ser Pro His Arg Asp Arg Asn Gly Val Val Asp Ser
890 895 900
Glu Ala Met Trp Lys Pro Ala Tyr Asp Phe Leu Leu Thr Trp Ser
905 910 915
His Gln Ile Gly Asp Ser Tyr Arg Asp Val Ile Gln Glu Leu His
920 925 930
Leu Gly Leu Asp Lys Met Lys Asn Pro Ile Thr Lys Arg Trp Lys
935 940 945
His Leu Thr Gly Thr Leu Ile Leu Val Asn Ser Leu Asp Val Leu
950 955 960
Arg Ala Ala Ala Phe Ser Pro Ala Asp Gln Asp Asp Phe Val Ile
965 970 975

<210> 199
<211> 484
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:998756.3.orf1:2002JAN18

<400> 199
Gly Gly Gly Pro Met Lys Asp Cys Glu Tyr Ser Gln Ile Ser Thr
1 5 10 15
His Ser Ser Ser Pro Met Glu Ser Pro His Lys Lys Lys Lys Ile
20 25 30
Ala Ala Arg Arg Lys Trp Glu Val Phe Pro Gly Arg Asn Lys Phe
35 40 45
Phe Cys Asn Gly Arg Ile Met Met Ala Arg Gln Thr Gly Val Phe
50 55 60
Tyr Leu Thr Leu Val Leu Ile Leu Val Thr Ser Gly Leu Phe Phe
65 70 75
Ala Phe Asp Cys Pro Tyr Leu Ala Val Lys Ile Thr Pro Ala Ile
80 85 90
Pro Ala Val Ala Gly Ile Leu Phe Phe Phe Val Met Gly Thr Leu
95 100 105
Leu Arg Thr Ser Phe Ser Asp Pro Gly Val Leu Pro Arg Ala Thr
110 115 120
Pro Asp Glu Ala Ala Asp Leu Glu Arg Gln Ile Asp Ile Ala Asn
125 130 135
Gly Thr Ser Ser Gly Gly Tyr Arg Pro Pro Pro Arg Thr Lys Glu
140 145 150
Val Ile Ile Asn Gly Gln Thr Val Lys Leu Lys Tyr Cys Phe Thr

155 160 165
Cys Lys Ile Phe Arg Pro Pro Arg Ala Ser His Cys Ser Leu Cys
170 175 180
Asp Asn Cys Val Glu Arg Phe Asp His His Cys Pro Trp Val Gly
185 190 195
Asn Cys Val Gly Lys Arg Asn Tyr Arg Phe Phe Tyr Met Phe Ile
200 205 210
Leu Ser Leu Ser Phe Leu Thr Val Phe Ile Phe Ala Phe Val Ile
215 220 225
Thr His Val Ile Leu Arg Ser Gln Gln Thr Gly Phe Leu Asn Ala
230 235 240
Leu Lys Asp Ser Pro Ala Ser Val Leu Glu Ala Val Val Cys Phe
245 250 255
Phe Ser Val Trp Ser Ile Val Gly Leu Ser Gly Phe His Thr Tyr
260 265 270
Leu Ile Ser Ser Asn Gln Thr Thr Asn Glu Asp Ile Lys Gly Ser
275 280 285
Trp Ser Asn Lys Arg Gly Lys Glu Asn Tyr Asn Pro Tyr Ser Tyr
290 295 300
Gly Asn Ile Phe Thr Asn Cys Cys Val Ala Leu Cys Gly Pro Ile
305 310 315
Ser Pro Ser Leu Ile Asp Arg Arg Gly Tyr Ile Gln Pro Asp Thr
320 325 330
Pro Gln Pro Ala Ala Pro Ser Asn Gly Ile Thr Met Tyr Gly Ala
335 340 345
Thr Gln Ser Gln Ser Asp Met Cys Asp Gln Asp Gln Cys Ile Gln
350 355 360
Ser Thr Lys Phe Val Leu Gln Ala Ala Ala Thr Pro Leu Leu Gln
365 370 375
Ser Glu Pro Ser Leu Thr Ser Asp Glu Leu His Leu Pro Gly Lys
380 385 390
Pro Gly Leu Gly Thr Pro Cys Ala Ser Leu Thr Leu Gly Pro Pro
395 400 405
Thr Pro Pro Ala Ser Met Pro Asn Leu Ala Glu Ala Thr Leu Ala
410 415 420
Asp Val Met Pro Arg Lys Asp Glu His Met Gly His Gln Phe Leu
425 430 435
Thr Pro Asp Glu Ala Pro Ser Pro Pro Arg Leu Leu Ala Ala Gly
440 445 450
Ser Pro Leu Ala His Ser Arg Thr Met His Val Leu Gly Leu Ala
455 460 465
Ser Gln Asp Ser Leu His Glu Asp Ser Val Arg Gly Leu Val Lys
470 475 480
Leu Ser Ser Val

<210> 200
<211> 275
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:103460.28.orf2:2002JAN18

<400> 200
Gln Arg His Gly His Met Pro Gln Ala Phe Leu Leu Gly Ser Ile
1 5 10 15
His Glu Pro Ala Gly Ala Leu Met Glu Pro Gln Pro Cys Pro Gly
20 25 30
Ser Leu Ala Glu Ser Phe Leu Glu Glu Glu Leu Arg Leu Asn Ala
35 40 45
Glu Leu Ser Gln Leu Gln Phe Ser Glu Pro Val Gly Ile Ile Tyr

```
                    50                          55                          60
Asn Pro Val Glu Tyr Ala Trp Glu Pro His Arg Asn Tyr Val Thr
                    65                          70                          75
Arg Tyr Cys Gln Gly Pro Lys Glu Val Leu Phe Leu Gly Met Asn
                    80                          85                          90
Pro Gly Pro Phe Gly Met Ala Gln Thr Gly Val Pro Phe Gly Glu
                    95                          100                         105
Val Ser Met Val Arg Asp Trp Leu Gly Ile Val Gly Pro Val Leu
                    110                         115                         120
Thr Pro Pro Gln Glu His Pro Lys Arg Pro Val Leu Gly Leu Glu
                    125                         130                         135
Cys Pro Gln Ser Glu Val Ser Gly Ala Arg Phe Trp Gly Phe Phe
                    140                         145                         150
Arg Asn Leu Cys Gly Gln Pro Glu Val Phe Phe His His Cys Phe
                    155                         160                         165
Val His Asn Leu Cys Pro Leu Leu Phe Leu Ala Pro Ser Gly Arg
                    170                         175                         180
Asn Leu Thr Pro Ala Glu Leu Pro Ala Lys Gln Arg Glu Gln Leu
                    185                         190                         195
Leu Gly Ile Cys Asp Ala Ala Leu Cys Arg Gln Val Gln Leu Leu
                    200                         205                         210
Gly Val Arg Leu Val Val Gly Val Gly Arg Leu Ala Glu Gln Arg
                    215                         220                         225
Ala Arg Arg Ala Leu Ala Gly Leu Met Pro Glu Val Gln Val Glu
                    230                         235                         240
Gly Leu Leu His Pro Ser Pro Arg Asn Pro Gln Ala Asn Lys Gly
                    245                         250                         255
Trp Glu Ala Val Ala Lys Glu Arg Leu Asn Glu Leu Gly Leu Leu
                    260                         265                         270
Pro Leu Leu Leu Lys
                    275
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<210> 201
<211> 245
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:1501505.19.orf1:2002JAN18

<400> 201

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Lys Ala Phe Ala Ser Gln Asn Asn Tyr Arg Ile Asp Ala Asn Gln
 1              5                   10                  15
Glu Leu Leu Ala Ile Gly Leu Thr Asn Met Leu Gly Ser Leu Val
                20                  25                  30
Ser Ser Tyr Pro Val Thr Gly Ser Phe Gly Arg Thr Ala Val Asn
                35                  40                  45
Ala Gln Ser Gly Val Cys Thr Pro Ala Gly Gly Leu Val Thr Gly
                50                  55                  60
Val Leu Val Leu Leu Ser Leu Asp Tyr Leu Thr Ser Leu Phe Tyr
                65                  70                  75
Tyr Ile Pro Lys Ser Ala Leu Ala Ala Val Ile Ile Met Ala Val
                80                  85                  90
Ala Pro Leu Phe Asp Thr Lys Ile Phe Arg Thr Leu Trp Arg Val
                95                  100                 105
Lys Arg Leu Asp Leu Leu Pro Leu Cys Val Thr Phe Leu Leu Cys
                110                 115                 120
Phe Trp Glu Val Gln Tyr Gly Ile Leu Ala Gly Ala Leu Val Ser
                125                 130                 135
Leu Leu Met Leu Leu His Ser Ala Ala Arg Pro Glu Thr Lys Val
                140                 145                 150
Ser Glu Gly Pro Val Leu Val Leu Gln Pro Ala Ser Gly Leu Ser
```

```
                    155                     160                     165
Phe Pro Ala Met Glu Ala Leu Arg Glu Glu Ile Leu Ser Arg Ala
                170                     175                     180
Leu Glu Gly Ala Trp Ala Gly Val Lys Cys Pro Arg His Ala Ala
                185                     190                     195
Trp Ser Trp Ser Ala Pro Met Ser Ala Ala Ser Thr Thr Leu Trp
                200                     205                     210
Cys Trp Asp Ser Ala Ser Ser Ser Arg Thr Ser Arg Ser Arg Ala
                215                     220                     225
Ser Pro Trp Pro Leu Trp Ala Cys Arg Ser Pro Phe Ser Val Ser
                230                     235                     240
Cys Cys Pro Leu Thr
                245
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<210> 202
<211> 247
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:233444.9.orf2:2002JAN18

<400> 202

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Ser Val Ser Cys Leu Val Tyr Met Thr Lys Gly Thr Leu Ala Phe
  1               5                  10                  15
Ser Asn Ala Trp Thr Tyr Leu Val Ile Ile Asn Asn Met Ser Gln
                 20                  25                  30
Leu Phe Ala Met Tyr Cys Leu Leu Leu Phe Tyr Lys Val Leu Lys
                 35                  40                  45
Glu Glu Leu Ser Pro Ile Gln Pro Val Gly Lys Phe Leu Cys Val
                 50                  55                  60
Lys Leu Val Val Phe Val Ser Phe Trp Gln Ala Val Val Ile Ala
                 65                  70                  75
Leu Leu Val Lys Val Gly Val Ile Ser Glu Lys His Thr Trp Glu
                 80                  85                  90
Trp Gln Thr Val Glu Ala Val Ala Thr Gly Leu Gln Asp Phe Ile
                 95                 100                 105
Ile Cys Ile Glu Met Phe Leu Ala Ala Ile Ala His His Tyr Thr
                110                 115                 120
Phe Ser Tyr Lys Pro Tyr Val Gln Glu Ala Glu Glu Gly Ser Cys
                125                 130                 135
Phe Asp Ser Phe Leu Ala Met Trp Asp Val Ser Asp Ile Arg Asp
                140                 145                 150
Asp Ile Ser Glu Gln Val Arg His Val Gly Arg Thr Val Arg Gly
                155                 160                 165
His Pro Arg Lys Lys Leu Phe Pro Glu Asp Gln Asp Gln Asn Glu
                170                 175                 180
His Thr Ser Leu Leu Ser Ser Ser Ser Gln Asp Ala Ile Ser Ile
                185                 190                 195
Ala Ser Ser Met Pro Pro Ser Pro Met Gly His Tyr Gln Gly Phe
                200                 205                 210
Gly His Thr Val Thr Pro Gln Thr Thr Pro Thr Thr Ala Lys Ile
                215                 220                 225
Ser Asp Glu Ile Leu Ser Asp Thr Ile Gly Glu Lys Lys Glu Pro
                230                 235                 240
Ser Asp Lys Ser Val Asp Ser
                245
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<210> 203
<211> 749
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:234824.7.orf2:2002JAN18

<400> 203
Ser Gln Pro Ala His Leu Gly Ala Ile Arg Leu Ser Arg Ala Trp
1 5 10 15
Ala Gly Phe Leu Thr Leu Trp Leu Asp Asn Asn Arg Ile Arg Tyr
20 25 30
Leu Pro Asp Ser Ile Val Glu Leu Thr Gly Leu Glu Glu Leu Val
35 40 45
Leu Gln Gly Asn Gln Ile Ala Val Leu Pro Asp His Phe Gly Gln
50 55 60
Leu Ser Arg Val Gly Leu Trp Lys Ile Lys Asp Asn Pro Leu Ile
65 70 75
Gln Pro Pro Tyr Glu Val Cys Met Lys Gly Ile Pro Tyr Ile Ala
80 85 90
Ala Tyr Gln Lys Glu Leu Ala His Ser Gln Pro Ala Val Gln Pro
95 100 105
Arg Leu Lys Leu Leu Leu Met Gly His Lys Ala Ala Gly Lys Thr
110 115 120
Leu Leu Arg His Cys Leu Thr Glu Glu Arg Val Glu Gly Cys Pro
125 130 135
Gly Gly Gly Asp Lys Glu Lys Cys Tyr Pro Pro Ser Pro Pro Pro
140 145 150
Val Ser Lys Gly Ile Glu Val Thr Ser Trp Thr Ala Asp Ala Ser
155 160 165
Arg Gly Leu Arg Phe Ile Val Tyr Asp Leu Ala Gly Asp Glu Ser
170 175 180
Tyr Glu Val Ile Gln Pro Phe Phe Leu Ser Pro Gly Ala Leu Tyr
185 190 195
Val Leu Val Val Asn Leu Ala Thr Tyr Glu Pro Arg His Phe Pro
200 205 210
Thr Thr Val Gly Ser Phe Leu His Arg Val Gly Ala Arg Val Pro
215 220 225
His Ala Val Val Cys Ile Val Gly Thr His Ala Asp Leu Cys Gly
230 235 240
Glu Arg Glu Leu Glu Glu Lys Cys Leu Asp Ile His Arg Gln Ile
245 250 255
Ala Leu Gln Glu Lys His Asp Ala Glu Gly Leu Ser Arg Leu Ala
260 265 270
Lys Val Val Asp Glu Ala Leu Ala Arg Asp Phe Glu Leu Arg Ser
275 280 285
Ala Ser Pro His Ala Ala Tyr Tyr Gly Val Ser Asp Lys Asn Leu
290 295 300
Arg Arg Arg Lys Ala His Phe Gln Tyr Leu Leu Asn His Arg Leu
305 310 315
Gln Ile Leu Ser Pro Val Leu Pro Val Ser Cys Arg Asp Pro Arg
320 325 330
His Leu Arg Arg Leu Arg Asp Lys Leu Leu Ser Val Ala Glu His
335 340 345
Arg Glu Ile Phe Pro Asn Leu His Arg Val Leu Pro Arg Ser Trp
350 355 360
Gln Val Leu Glu Glu Leu His Phe Gln Pro Pro Gln Ala Gln Arg
365 370 375
Leu Trp Leu Ser Trp Trp Asp Ser Ala Arg Leu Gly Leu Gln Ala
380 385 390
Gly Leu Thr Glu Asp Arg Leu Gln Ser Ala Leu Ser Tyr Leu His
395 400 405
Glu Ser Gly Lys Leu Leu Tyr Phe Glu Asp Ser Pro Ala Leu Lys
410 415 420
Glu His Val Phe His Asn Leu Thr Arg Leu Ile Asp Ile Leu Asn
425 430 435

```
Val Phe Phe Gln Arg Asp Pro Ser Leu Leu Leu His Lys Leu Leu
                440                 445                 450
Leu Gly Thr Ser Gly Glu Gly Lys Ala Glu Gly Glu Ser Ser Pro
                455                 460                 465
Pro Met Ala Arg Ser Thr Pro Ser Gln Glu Leu Leu Arg Ala Thr
                470                 475                 480
Gln Leu His Gln Tyr Val Glu Gly Phe Leu Leu His Gly Leu Leu
                485                 490                 495
Pro Ala His Val Ile Arg Leu Leu Leu Lys Pro His Val Gln Ala
                500                 505                 510
Gln Gln Asp Leu Gln Leu Leu Leu Glu Leu Leu Glu Lys Met Gly
                515                 520                 525
Leu Cys Tyr Cys Leu Asn Lys Pro Lys Gly Lys Pro Leu Asn Gly
                530                 535                 540
Ser Thr Ala Trp Tyr Lys Phe Pro Cys Tyr Val Gln Asn Glu Val
                545                 550                 555
Pro His Ala Glu Ala Trp Ile Asn Gly Thr Asn Leu Ala Gly Gln
                560                 565                 570
Ser Phe Val Ala Glu Gln Leu Gln Ile Glu Tyr Ser Phe Pro Phe
                575                 580                 585
Thr Phe Pro Pro Gly Leu Phe Ala Arg Tyr Ser Val Gln Ile Asn
                590                 595                 600
Ser His Val Val His Arg Ser Asp Gly Lys Phe Gln Ile Phe Ala
                605                 610                 615
Tyr Arg Gly Lys Val Pro Val Val Val Ser Tyr Arg Pro Ala Arg
                620                 625                 630
Gly Val Leu Gln Pro Asp Thr Leu Ser Ile Ala Ser His Ala Ser
                635                 640                 645
Leu Pro Asn Ile Trp Thr Ala Trp Gln Ala Ile Thr Pro Leu Val
                650                 655                 660
Glu Glu Leu Asn Val Leu Leu Gln Glu Trp Pro Gly Leu His Tyr
                665                 670                 675
Thr Val His Ile Leu Cys Ser Lys Cys Leu Lys Arg Gly Ser Pro
                680                 685                 690
Asn Pro His Ala Phe Pro Gly Glu Leu Leu Ser Gln Pro Arg Pro
                695                 700                 705
Glu Gly Val Ala Glu Ile Ile Cys Pro Lys Asn Gly Ser Glu Arg
                710                 715                 720
Val Asn Val Ala Leu Val Tyr Pro Pro Thr Pro Thr Val Ile Ser
                725                 730                 735
Pro Cys Ser Lys Lys Asn Val Gly Glu Lys His Arg Asn Gln
                740                 745
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<210> 204
<211> 330
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:235708.23.orf1:2002JAN18

<400> 204

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Gly Pro Arg Ser Pro Leu Pro Ile Leu Pro Pro Ala Arg Gly Ser
 1               5                  10                  15
Gly His Leu Met Ala Leu Ala Gly Thr Gln Val Gly Pro Pro Pro
                20                  25                  30
Gln Glu Arg Ala Pro Glu Pro Ile Gly Arg Ala Trp Gly Pro Pro
                35                  40                  45
Gly Ile Thr Gln Pro Ser Ala Pro Gly Ala Thr Val Gly Arg Arg
                50                  55                  60
Val Ser Val Ala Ala Gly Pro Trp Leu His Gly Pro His Gly Ser
                65                  70                  75
```

Cys Glu Trp Val Arg Leu Pro Gly Ser Gly Asp Arg Gln Arg Thr
80 85 90
Asp Pro Arg Leu Gly Ser Trp Arg Glu Gly Arg Arg Gly Ala Gly
95 100 105
Gln Pro Gly Ser Asp Thr Val Ser Ser Ser Gly Arg Arg Arg Pro
110 115 120
Ala Gly Ser Thr Gln Ala Gly Arg Gly Trp Ala Ser Leu Glu Pro
125 130 135
Ala Thr Ala Leu Val Gly Thr Trp Arg Arg Ala His Val Ser Pro
140 145 150
His Ala Ser His Arg Gly Ala Leu Ala Arg Arg Pro Ala Arg Gly
155 160 165
Ala Cys Ala Trp Asp Gly Ser Gln Asn Gln Arg Ala Pro Val Arg
170 175 180
Leu Ala Ser Thr Val Gly Leu Trp Glu Ser Leu Leu Phe Ile Phe
185 190 195
Lys His Leu Gly Phe Ser Thr Gly Ser Trp Leu Leu Phe Pro Gln
200 205 210
Gly Met Ser Leu Arg Ser Arg Thr Arg Trp Gly Ser Gln Glu Ala
215 220 225
Ala Ala Gln Ser Leu His Ala Gly Lys Gly Ser His Leu Ser Gly
230 235 240
Val Gly Ser Leu Val Val Gln Gly Ser Ala Gly Gln Ser Leu Gly
245 250 255
Cys Ala Ile Thr Ala Thr Ala Phe Leu Leu Gly Ala Ser Thr Ser
260 265 270
His Pro Lys Thr Gly Pro Cys Ala Ser Pro Thr Arg Gly Glu Arg
275 280 285
Thr Arg Pro Arg Arg Gln Gly Pro Glu Tyr Leu Gly Gly Gly Asp
290 295 300
Thr Pro Arg Gly His Arg Gly Gly Ser His Leu Gly Thr Cys Leu
305 310 315
Leu Pro Phe Ser Ser Ser Ser Thr Cys Gln Val Gly Pro Trp Val
320 325 330

<210> 205
<211> 301
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:236649.14.orf1:2002JAN18

<400> 205
Arg Ala Trp Gly Pro Leu Leu Ser Ile Gly Gly Gly Gln Arg Gln
1 5 10 15
His Gln Arg Leu Val Glu Gln Tyr Arg Glu Gln Ser Trp Met Thr
20 25 30
Met Ala Asn Leu Glu Lys Glu Leu Gln Glu Met Glu Ala Arg Tyr
35 40 45
Glu Lys Glu Phe Gly Asp Gly Ser Asp Glu Asn Glu Met Glu Glu
50 55 60
His Glu Leu Lys Asp Glu Glu Asp Gly Lys Asp Ser Asp Glu Ala
65 70 75
Glu Asp Ala Glu Leu Tyr Asp Asp Leu Tyr Cys Pro Ala Cys Asp
80 85 90
Lys Ser Phe Lys Thr Glu Lys Ala Met Lys Asn His Glu Lys Ser
95 100 105
Lys Lys His Arg Glu Met Val Ala Leu Leu Lys Gln Gln Leu Glu
110 115 120
Glu Glu Glu Glu Asn Phe Ser Arg Pro Gln Ile Asp Glu Asn Pro

```
                    125                     130                     135
Leu Asp Asp Asn Ser Glu Glu Glu Met Glu Asp Ala Pro Lys Gln
                140                     145                     150
Lys Leu Ser Lys Lys Gln Lys Lys Lys Lys Gln Lys Pro Ala Gln
                155                     160                     165
Asn Tyr Asp Asp Asn Phe Asn Val Asn Gly Pro Gly Glu Gly Val
                170                     175                     180
Lys Val Asp Pro Glu Asp Thr Asn Leu Asn Gln Asp Ser Ala Lys
                185                     190                     195
Glu Leu Glu Asp Ser Pro Gln Glu Asn Val Ser Val Thr Glu Ile
                200                     205                     210
Ile Lys Pro Cys Asp Asp Pro Lys Ser Glu Ala Lys Ser Val Pro
                215                     220                     225
Lys Pro Lys Gly Lys Lys Thr Lys Asp Met Lys Lys Pro Val Arg
                230                     235                     240
Val Pro Ala Glu Pro Gln Thr Met Ser Val Leu Ile Ser Cys Thr
                245                     250                     255
Thr Cys His Ser Glu Phe Pro Ser Arg Asn Lys Leu Phe Asp His
                260                     265                     270
Leu Lys Ala Thr Gly His Ala Arg Ala Pro Ser Ser Ser Ser Leu
                275                     280                     285
Asn Ser Ala Thr Ser Ser Gln Ser Lys Lys Glu Lys Arg Lys Asn
                290                     295                     300
Arg
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<210> 206
<211> 213
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:332474.7.orf1:2002JAN18

<400> 206

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Ala Thr Asp Thr Ser Asp Thr Arg Cys Gly Gly Arg Arg Ser Gly
 1              5                   10                  15
Ser Gly Ala Val Pro Ser Ala Ser Val Gly Arg His Pro Leu Ala
                20                  25                  30
Ala Glu Pro Ala Leu His Trp Gly Pro Trp Gly Arg Leu Leu Gln
                35                  40                  45
Thr Ser Leu Arg Val Val Gly Cys Cys Arg Val Gly Leu Gly Asp
                50                  55                  60
Ala Thr Gly Ser Gly Ser Gly Ala Ala Ala Gly Pro Ser Ser His
                65                  70                  75
Cys Pro Ser Ser Asp Pro Thr Val Leu Trp Lys Leu Val Gln Gly
                80                  85                  90
Thr Cys His Cys Asp His Leu Asp Ala Asp Thr Cys Phe Pro Thr
                95                  100                 105
Thr Ala Arg Lys Asn His Gly Pro Gly Ser Leu Ser Phe Gly Asp
                110                 115                 120
Val Ala Val Gly Phe Thr Arg Lys Glu Trp Leu Ala Ala Gly Pro
                125                 130                 135
Gly Ala Glu Asp Pro Val Pro Gly Cys Asn Ala Gly Glu Leu Gln
                140                 145                 150
Pro Pro Ala Leu Cys Gly Leu Asn Cys Leu Leu Ala Trp Lys Ala
                155                 160                 165
Gln Leu Ala Gln His Lys Ser Phe Asn Arg Phe Ser Pro Arg Gly
                170                 175                 180
Cys Gln Val Ser Lys Pro Ala Val Ile Ser Ser Leu Glu Gln Gly
                185                 190                 195
Lys Glu Pro Trp Met Glu Glu Glu Glu Ile Arg Thr Trp Ser Phe
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200 205 210
Pro Glu Ser

<210> 207
<211> 322
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: LG:335727.8.orf2:2002JAN18

<400> 207
Lys Ala Gly Gly Thr Asn Cys Gln Cys Leu Glu Ser Gly Ser Arg
1 5 10 15
Leu Pro Phe Leu Gly Ala Leu Gly Val Ala Val Ala Val Ala Glu
20 25 30
Ile Gly Cys Thr Met Ser Ala Phe Glu Lys Pro Gln Ile Ile Ala
35 40 45
His Ile Gln Lys Gly Phe Asn Tyr Thr Val Phe Asp Cys Lys Trp
50 55 60
Val Pro Cys Ser Ala Lys Phe Val Thr Met Gly Asn Phe Ala Arg
65 70 75
Gly Thr Gly Val Ile Gln Leu Tyr Glu Ile Gln His Gly Asp Leu
80 85 90
Lys Leu Leu Arg Glu Ile Glu Lys Ala Lys Pro Ile Lys Cys Gly
95 100 105
Thr Phe Gly Ala Thr Ser Leu Gln Gln Arg Tyr Leu Ala Thr Gly
110 115 120
Asp Phe Gly Gly Asn Leu His Ile Trp Asn Leu Glu Ala Pro Glu
125 130 135
Met Pro Val Tyr Ser Val Lys Gly His Lys Glu Ile Ile Asn Ala
140 145 150
Ile Asp Gly Ile Gly Gly Leu Gly Ile Gly Glu Gly Ala Pro Glu
155 160 165
Ile Val Thr Gly Ser Arg Asp Gly Thr Val Lys Val Trp Asp Pro
170 175 180
Arg Gln Lys Asp Asp Pro Val Ala Asn Met Glu Pro Val Gln Gly
185 190 195
Glu Asn Lys Arg Asp Cys Trp Thr Val Ala Phe Gly Asn Ala Tyr
200 205 210
Asn Gln Glu Glu Arg Val Val Cys Ala Gly Tyr Asp Asn Gly Asp
215 220 225
Ile Lys Leu Phe Asp Leu Arg Asn Met Ala Leu Arg Trp Glu Thr
230 235 240
Asn Ile Lys Asn Gly Val Cys Ser Leu Glu Phe Asp Arg Lys Asp
245 250 255
Ile Ser Met Asn Lys Leu Val Ala Thr Ser Leu Glu Gly Lys Phe
260 265 270
His Val Phe Asp Met Arg Thr Gln His Pro Thr Lys Gly Phe Ala
275 280 285
Ser Val Ser Glu Lys Ala His Lys Ser Thr Val Trp Gln Val Arg
290 295 300
His Leu Pro Gln Asn Arg Glu Leu Phe Leu Thr Ala Gly Gly Ala
305 310 315
Gly Gly Leu His Leu Trp Lys
320

<210> 208
<211> 238
<212> PRT
<213> Homo sapiens

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<220>
<221> misc_feature
<223> Incyte ID No: LG:481983.1.orf3:2002JAN18

<400> 208
Ala Val Ser Leu Arg Cys Leu Gly Tyr Lys Leu Gly Ser Leu Leu
 1               5                  10                  15
Thr Thr Asn His Ser Phe Phe Phe Phe His Leu Gln Pro Leu Thr
                20                  25                  30
Thr Asp Leu His Tyr Tyr Tyr Ile Leu Glu Leu Ser Phe Tyr Trp
                35                  40                  45
Ser Leu Met Phe Ser Gln Phe Thr Asp Ile Lys Arg Lys Asp Phe
                50                  55                  60
Gly Ile Met Phe Leu His His Leu Val Ser Ile Phe Leu Ile Thr
                65                  70                  75
Phe Ser Tyr Val Asn Asn Met Ala Arg Val Gly Thr Leu Val Leu
                80                  85                  90
Cys Leu His Asp Ser Ala Asp Ala Leu Leu Glu Ala Ala Lys Met
                95                 100                 105
Ala Asn Tyr Ala Lys Phe Gln Lys Met Cys Asp Leu Leu Phe Val
               110                 115                 120
Met Phe Ala Val Val Phe Ile Thr Thr Arg Leu Gly Ile Phe Pro
               125                 130                 135
Leu Trp Val Leu Asn Thr Thr Leu Phe Glu Ser Trp Glu Ile Val
               140                 145                 150
Gly Pro Tyr Pro Ser Trp Trp Val Phe Asn Leu Leu Leu Leu Leu
               155                 160                 165
Val Gln Gly Leu Asn Cys Phe Trp Ser Tyr Leu Ile Val Lys Ile
               170                 175                 180
Ala Cys Lys Ala Val Ser Arg Gly Lys Ala Gly Lys Trp Asn Pro
               185                 190                 195
Tyr Met Cys Pro Arg Met Ile Glu Val Ile Leu Ser Leu Ala Gln
               200                 205                 210
Met Arg Arg Thr Gln Asn Leu Arg Glu Arg Ile Pro Thr Leu Arg
               215                 220                 225
Gln Pro Pro Met Gly Pro Val Val Pro Thr Gly Ile Ser
               230                 235
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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 2003/062379 A3

(54) Title: MOLECULES FOR DISEASE DETECTION AND TREATMENT

(57) Abstract: The present invention provides purified disease detection and treatment molecule polynucleotides (mddt). Also encompassed are the polypeptides (MDDT) encoded by mddt. The invention also provides for the use of mddt, or complements, oligonucleotides, or fragments thereof in diagnostic assays. The invention further provides for vectors and host cells containing mddt for the expression of MDDT. The invention additionally provides for the use of isolated and purified MDDT to induce antibodies and to screen libraries of compounds and the use of anti-MDDT antibodies in diagnostic assays. Also provided are microarrays containing mddt and methods of use.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US03/01363

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12N 15/11, 15/12, 15/00; C12Q 1/68; C07K 14/00, 14/435
US CL : 536/23.1, 23.5; 435/6, 320/1, 325, 252.3; 530/350; 514/12

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
U.S. : 536/23.1, 23.5; 435/6, 320/1, 325, 252.3; 530/350; 514/12

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Compugen, SEQ ID NOs: 1 and 105

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X --- Y	WO 01/53312 A1 (HYSEQ, INC.) 26 July 2001 (26.07.2001), compare SEQ ID NO: !, position 529-1305 to reference SEQ ID NO: 1215, positions 403-1179 and see alignment attached to the reference.	3 and 6-8 --- 16 and 20-26
X	EP 1033401 A2 (GENSET) 06 September 2000 (06.09.2000), compare SEQ ID NO: 105, positions 25-140 to SEQ ID NO: 7103, positions 1-116 and alignment attached to reference.	27

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search 26 August 2003 (26.08.2003)	Date of mailing of the international search report 05 DEC 2003
Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US Commissioner for Patents P.O. Box 1450 Alexandria, Virginia 22313-1450 Facsimile No.	Authorized officer James Martinell Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US03/01363

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.: Please See Continuation Sheet

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest ☒ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

PCT/US03/01363

Continuation of Box II Item 3:
1-10, 12, 13, 16, 17, and 19-28 to the extent that they include SEQ ID NO: 1 and 105